

From: McGarry, Sean
Sent: Wednesday, June 05, 2002 1:11 PM
To: STIC-Biotech/ChemLib
Subject: Sequence Search 09/599,220

Please,

For 09/599,220, a length limited search of SEQ ID NO: 1 and 2 (nucleotides < 50). Please do not search ESTs.

Thank You
Sean McGarry
AU 1635
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305-7028

Point of Contact:
Barb O'Bryen
Technical Information Specialist
STIC CM1 6A05 308-4291

	TYPE OF SEARCH:	VENDOR/COST(where applic.)
Searcher: <u>BOB</u>	NA Sequences: _____	STN: _____
Phone: _____	AA Sequences: _____	DIALOG: _____
Location: _____	Structures: _____	Questel/Orbit: _____
Date Picked Up: _____	Bibliographic: _____	DRLink: _____
Date Completed: <u>6-7-02</u>	Litigation: _____	Lexis/Nexis: _____
Searcher Prep/Review: _____	Full text: _____	Sequence Sys.: _____
Clerical: _____	Patent Family: _____	WWW/Internet: _____
Online time: _____	Other: _____	Other (specify): _____



GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 6, 2002, 16:03:19 ; Search time 1796.86 Seconds
(without alignments)
337.739 Million cell updates/sec

Title: US-09-599-220-2

Sequence: 1 aglccgtggtacgagcaggttggtgact 29

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 708260

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : GenEmbl:*
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6: gb_pat:*
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33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
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1	29	100.0	38	6	ARI25937	ARI25937 Sequence
2	29	100.0	38	6	I24304	I24304 Sequence 91
3	29	100.0	38	6	I49650	I49650 Sequence 2
4	29	100.0	38	6	I56644	I56644 Sequence 2
5	29	100.0	39	6	ARI40900	ARI40900 Sequence
6	29	100.0	39	6	ARI50850	ARI50850 Sequence
7	29	100.0	39	6	I65730	I65730 Sequence 90
8	29	100.0	39	6	I67962	I67962 Sequence 90
9	29	100.0	39	6	I90181	I90181 Sequence 88
10	19.8	68.3	30	6	ARI25877	ARI25877 Sequence
11	19.8	68.3	30	6	I24244	I24244 Sequence 31
12	19.4	66.9	30	6	ARI25890	ARI25890 Sequence
13	19.4	66.9	30	6	I24257	I24257 Sequence 44
14	19.4	66.9	30	6	ARI25893	ARI25893 Sequence
15	19	65.5	30	6	I24260	I24260 Sequence 47
16	18.8	64.8	30	6	ARI25875	ARI25875 Sequence
17	18.8	64.8	30	6	I24242	I24242 Sequence 29
18	17.4	60.0	47	6	ARI194776	ARI194776 Sequence
19	17.2	59.3	30	6	ARI25881	ARI25881 Sequence
20	17.2	59.3	30	6	I24248	I24248 Sequence 35
21	17	58.6	47	6	ARI194777	ARI194777 Sequence
22	16	55.2	30	6	ARI25889	ARI25889 Sequence
23	16	55.2	30	6	I24256	I24256 Sequence 43
24	15.8	54.5	30	6	ARI25878	ARI25878 Sequence
25	15.8	54.5	30	6	I24245	I24245 Sequence 32
26	15.8	54.5	50	6	AX236815	AX236815 Sequence
27	15	51.7	50	6	AXI59200	AXI59200 Sequence
28	14.8	51.0	29	6	I15689	I15689 Sequence 3
29	14.8	51.0	30	6	I11736	I11736 Sequence 7
30	14.8	51.0	37	6	E29444	E29444 Oligonucleo
31	14.6	50.3	21	6	A59112	A59112 Sequence 4
32	14.6	50.3	25	6	AR073593	AR073593 Sequence 64
33	14.6	50.3	25	6	A59172	A59172 Sequence
34	14.6	50.3	25	6	AR073653	AR073653 Sequence
35	14.6	50.3	38	6	ARI68778	ARI68778 Sequence
36	14.6	50.3	38	6	I27772	I27772 Sequence 4
37	14.4	49.7	21	6	AX096640	AX096640 Sequence
38	14.4	49.7	21	6	I00071	I00071 Sequence 3
39	14.2	49.0	21	6	AR009315	AR009315 Sequence
40	14.2	49.0	24	6	A59166	A59166 Sequence 58
41	14.2	49.0	24	6	AR073647	AR073647 Sequence
42	14.2	49.0	31	6	I38370	I38370 Sequence 2
43	14.2	49.0	45	10	KMU232758	AJ232758 Mus muscu
44	14.2	49.0	50	6	AXI90214	AXI90214 Sequence
45	14.2	49.0	50	9	HSTPE31D2	X84963 H.sapiens t

ALIGNMENTS

RESULT 1
LOCUS ARI25937 38 bp DNA
DEFINITION Sequence 279 from patent US 6177557.
ACCESSION ARI25937
VERSION ARI25937.1 GI:14111999
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS Janjic, N., Gold, L. and Tasset, D.
TITLE High affinity ligands of basic fibroblast growth factor and thrombin
JOURNAL Patent: US 6177557-A 279 23-JAN-2001;
FEATURES
source Location/Qualifiers
BASE COUNT 6 a 6 c 17 g 9 t
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Query Match 100.0%; Score 29; DB 6; Length 38;

Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 2 AGTCCTGTAGGCGCAGTTGGGTGACT 30

RESULT 2
LOCUS I24304 38 bp DNA
DEFINITION Sequence 91 from patent US 5543293.
ACCESSION I24304
VERSION I24304.1 GI:1604174
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 38)
AUTHORS Gold,L. and Tasset,D.
TITLE DNA ligands of thrombin
JOURNAL Patent: US 5543293-A 91 06-AUG-1996;
FEATURES
source Location/Qualifiers
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BASE COUNT 6 a 6 c 17 g 9 t
ORIGIN

Query Match 100.0%; Score 29; DB 6; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agtcctgttaggcaggttggtgact 29
Db 2 AGTCCTGTAGGCGCAGTTGGGTGACT 30

RESULT 3
LOCUS I49650 38 bp DNA
DEFINITION Sequence 2 from patent US 5641629.
ACCESSION I49650
VERSION I49650.1 GI:2471870
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 38)
AUTHORS Pitner,J.B., Malinowski,D.P., Vonk,G.P. and Gold,L.
TITLE Spectroscopically detectable nucleic acid ligands
JOURNAL Patent: US 5641629-A 2 24-JUN-1997;
FEATURES
source Location/Qualifiers
1..38
/organism="unknown"

BASE COUNT 6 a 6 c 17 g 9 t
ORIGIN

Query Match 100.0%; Score 29; DB 6; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agtcctgttaggcaggttggtgact 29
Db 2 AGTCCTGTAGGCGCAGTTGGGTGACT 30

RESULT 4
LOCUS I56644 38 bp DNA
DEFINITION Sequence 2 from patent US 5650275.
ACCESSION I56644

VERSION I56644.1 GI:2477057
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 38)
AUTHORS Pitner,J.Bruce., Malinowski,D.P., Vonk,G.P. and Gold,L.
TITLE Target detection method using spectroscopically detectable nucleic acid ligands
JOURNAL Patent: US 5650275-A 2 22-JUN-1997;
FEATURES
source Location/Qualifiers
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/organism="unknown"

BASE COUNT 6 a 6 c 17 g 9 t
ORIGIN

Query Match 100.0%; Score 29; DB 6; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agtcctgttaggcaggttggtgact 29
Db 2 AGTCCTGTAGGCGCAGTTGGGTGACT 30

RESULT 5
LOCUS AR140900 39 bp DNA
DEFINITION Sequence 177 from patent US 6207816.
ACCESSION AR140900
VERSION AR140900.1 GI:14483396
KEYWORDS
SOURCE Unknown.

REFERENCE 1 (bases 1 to 39)
AUTHORS Gold,L., Janjic,N. and Pagratis,N.
TITLE High affinity oligonucleotide ligands to growth factors
JOURNAL Patent: US 6207816-A 177 27-MAR-2001;
FEATURES
source Location/Qualifiers
1..39
/organism="unknown"

BASE COUNT 6 a 6 c 17 g 10 t
ORIGIN

Query Match 100.0%; Score 29; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agtcctgttaggcaggttggtgact 29
Db 2 AGTCCTGTAGGCGCAGTTGGGTGACT 30

RESULT 6
LOCUS AR150850 39 bp DNA
DEFINITION Sequence 88 from patent US 6229002.
ACCESSION AR150850
VERSION AR150850.1 GI:15115441
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 39)
AUTHORS Janjic,N. and Gold,L.
TITLE Platelet derived growth factor (PDGF) nucleic acid ligand complexes
JOURNAL Patent: US 6229002-A 88 08-MAY-2001;
FEATURES
source Location/Qualifiers
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/organism="unknown"

BASE COUNT 6 a 6 c 17 g 10 t
ORIGIN

Query Match 100.0%; Score 29; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 agtccgtgtagggcaggttgaggtagact 29
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Db 2 AGTCGCTGTAGGCGCAGGTTGGGCTGACT 30

RESULT 7
LOCUS 165730 39 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 90 from patent US 5668264.
ACCESSION 165730
VERSION 165730.1 GI:2482300
KEYWORDS

SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 39)
AUTHORS Janjic,N. and Gold,L.
TITLE High affinity PDGF nucleic acid ligands
JOURNAL Patent: US 5668264-A 90 16-SEP-1997;
FEATURES Location/Qualifiers
source 1..39
/organism="unknown"

BASE COUNT 6 a 6 c 17 g 10 t
ORIGIN

Query Match 100.0%; Score 29; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 agtccgtgtagggcaggttgaggtagact 29
|||||
Db 2 AGTCGCTGTAGGCGCAGGTTGGGCTGACT 30

RESULT 8
LOCUS 167962 39 bp DNA linear PAT 04-FEB-1998
DEFINITION Sequence 90 from patent US 5674685.
ACCESSION 167962
VERSION 167962.1 GI:2830084
KEYWORDS

SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 39)
AUTHORS Janjic,N. and Gold,L.
TITLE High affinity PDGF nucleic acid ligands
JOURNAL Patent: US 5674685-A 90 07-OCT-1997;
FEATURES Location/Qualifiers
source 1..39
/organism="unknown"

BASE COUNT 6 a 6 c 17 g 10 t
ORIGIN

Query Match 100.0%; Score 29; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 agtccgtgtagggcaggttgaggtagact 29
|||||
Db 2 AGTCGCTGTAGGCGCAGGTTGGGCTGACT 30

RESULT 9
LOCUS 190181 39 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 88 from patent US 5723594.
ACCESSION 190181
VERSION 190181.1 GI:3410121
KEYWORDS

SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 39)
AUTHORS Janjic,N. and Gold,L.
TITLE High affinity PDGF nucleic acid ligands
JOURNAL Patent: US 5723594-A 88 03-MAR-1998;
FEATURES Location/Qualifiers
source 1..39
/organism="unknown"

BASE COUNT 6 a 6 c 17 g 10 t
ORIGIN

Query Match 100.0%; Score 29; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 agtccgtgtagggcaggttgaggtagact 29
|||||
Db 2 AGTCGCTGTAGGCGCAGGTTGGGCTGACT 30

RESULT 10
LOCUS ARI25877 30 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 219 from patent US 6177557.
ACCESSION ARI25877
VERSION ARI25877.1 GI:14111939
KEYWORDS

SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Janjic,N., Gold,L. and Tasset,D.
TITLE High affinity ligands of basic fibroblast growth factor and thrombin
JOURNAL Patent: US 6177557-A 219 23-JAN-2001;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"

BASE COUNT 5 a 5 c 14 g 6 t
ORIGIN

Query Match 68.3%; Score 19.8; DB 6; Length 30;
Best Local Similarity 91.3%; Pred. No. 1.9e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 ccgtgtagggcaggttgaggtagact 26
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Db 5 CCGTGTAGGCGTAGCATGGCGGTG 27

RESULT 11
LOCUS I24244 30 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 31 from patent US 5543293.
ACCESSION I24244
VERSION I24244.1 GI:1604114
KEYWORDS

SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Gold,L. and Tasset,D.

TITLE DNA ligands of thrombin
JOURNAL Patent: US 5543293-A 31 06-AUG-1996;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"

BASE COUNT 5 a 5 c 14 g 6 t
ORIGIN

Query Match 68.3%; Score 19.8; DB 6; Length 30;
Best Local Similarity 91.3%; Pred. No. 1.9e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ccctgttaggcaggttgaggtg 26
Db 5 ccctgttaggcaggttgaggtg 27

RESULT 12
125890

DEFINITION AR125890 30 bp DNA linear PAT 16-MAY-2001
ACCESSION AR125890
VERSION AR125890.1 GI:14111952

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 30)

AUTHORS Janjic,N., Gold,L., and Tasset,D.
TITLE High affinity ligands of basic fibroblast growth factor and thrombin

JOURNAL Patent: US 6177557-A 232 23-JAN-2001;

FEATURES Location/Qualifiers

source 1..30

/organism="unknown"

BASE COUNT 4 a 3 c 14 g 9 t
ORIGIN

Query Match 66.9%; Score 19.4; DB 6; Length 30;
Best Local Similarity 95.2%; Pred. No. 2.8e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ccttgtaggcaggttgaggtg 25

Db 9 CGTGTAGGCTAGGTGGGCT 29

RESULT 13

LOCUS 124257 30 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 44 from patent US 5543293.
ACCESSION 124257

VERSION 124257.1 GI:1604127

KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 30)

AUTHORS Gold,L., and Tasset,D.

TITLE DNA ligands of thrombin

JOURNAL Patent: US 5543293-A 44 06-AUG-1996;

FEATURES Location/Qualifiers

source 1..30

/organism="unknown"

BASE COUNT 4 a 3 c 14 g 9 t
ORIGIN

Query Match 66.9%; Score 19.4; DB 6; Length 30;
Best Local Similarity 95.2%; Pred. No. 2.8e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ccttgtaggcaggttgaggtg 25
Db 9 CGTGTAGGCTAGGTGGGCT 29

RESULT 14

LOCUS AR125893 30 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 235 from patent US 6177557.
ACCESSION AR125893

VERSION AR125893.1 GI:14111955

KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 30)

AUTHORS Janjic,N., Gold,L., and Tasset,D.

TITLE High affinity ligands of basic fibroblast growth factor and thrombin

JOURNAL Patent: US 6177557-A 235 23-JAN-2001;

FEATURES Location/Qualifiers

source 1..30

/organism="unknown"

BASE COUNT 4 a 3 c 13 g 10 t
ORIGIN

Query Match 65.5%; Score 19; DB 6; Length 30;
Best Local Similarity 81.5%; Pred. No. 4e+03;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 tccctgttaggcaggttgaggtgact 29

Db 4 TGCCTGTAGGCTAGGTGTGTCATT 30

RESULT 15

LOCUS 124260 30 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 47 from patent US 5543293.
ACCESSION 124260

VERSION 124260.1 GI:1604130

KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 30)

AUTHORS Gold,L., and Tasset,D.

TITLE DNA ligands of thrombin

JOURNAL Patent: US 5543293-A 47 06-AUG-1996;

FEATURES Location/Qualifiers

source 1..30

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BASE COUNT 4 a 3 c 13 g 10 t
ORIGIN

Query Match 65.5%; Score 19; DB 6; Length 30;
Best Local Similarity 81.5%; Pred. No. 4e+03;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 tccctgttaggcaggttgaggtgact 29

Db 4 TGCCTGTAGGCTAGGTGTGTCATT 30

Search completed: June 6, 2002, 16:03:21
Job time: 1822 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 6, 2002, 16:08:47 ; Search time 234.25 Seconds
(Without alignments)
212.553 Million cell updates/sec

Title: US-09-599-220-2

perfect score: 29
Sequence: 1 agtcggtgtagggcgaggttgggtgact 29

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

total number of hits satisfying chosen parameters: 1905168

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	29	22 AAC91745	Thrombin-binding a
2	29	100.0	37	24 AAS16530	Thrombin specific,
3	29	100.0	37	24 AAS16540	Thrombin specific,
4	29	100.0	38	16 AAQ98404	Truncated SLEK de
5	29	100.0	38	17 AAT86554	Spectroscopically
6	29	100.0	38	17 AAT86554	Thrombin ligand fo
7	29	100.0	38	18 AAT85812	Thrombin-binding
8	29	100.0	38	18 AAT80049	Thrombin binding 1
9	29	100.0	38	22 AAT70817	Thrombin high affi

10	29	100.0	39	20 AAX87088	DNA ligand T39 to
11	29	100.0	42	24 AAS16537	Thrombin specific,
12	29	100.0	43	24 AAS16537	Thrombin specific,
13	19.8	68.3	30	16 AAT00205	Thrombin DNA ligand
14	19.8	68.3	30	22 AAT70757	Thrombin high affi
15	19.4	66.9	30	16 AAT00218	Thrombin DNA ligand
16	19.4	66.9	30	22 AAT70770	Thrombin high affi
17	19	66.5	30	16 AAT00221	Thrombin DNA ligand
18	19	65.5	30	22 AAT70773	Thrombin high affi
19	18.8	64.8	30	16 AAT00203	Thrombin DNA ligand
20	18.8	64.8	30	22 AAT70755	Thrombin high affi
21	17.4	60.0	47	23 AAT88406	CNS disorder-relat
22	17.2	59.3	30	16 AAT00209	Thrombin DNA ligand
23	17.2	59.3	30	22 AAT70761	Thrombin high affi
24	17	58.6	47	23 AAT88407	CNS disorder-relat
25	16.4	55.6	50	22 AAL31191	Human SNP oligonuc
26	16	55.2	30	16 AAT00217	Thrombin DNA ligand
27	16	55.2	30	22 AAT70769	Thrombin high affi
28	15.8	54.5	30	16 AAT00206	Thrombin DNA ligand
29	15.8	54.5	30	22 AAT70758	Thrombin high affi
30	15.8	54.5	50	22 AAS44248	Neisseria meningit
31	15	51.7	32	24 AAS16529	Thrombin specific,
32	15	51.7	35	24 AAS16535	Thrombin specific,
33	15	51.7	38	24 AAS16532	Thrombin specific,
34	15	51.7	50	22 AAT75587	Human silent SNP c
35	15	51.7	50	22 AAT75587	Human silent SNP c
36	14.8	51.0	30	14 AAO41753	Human vitamin D re
37	14.8	51.0	37	21 AAT56511	Human SNP oligonuc
38	14.8	51.0	50	22 AAL30621	Sequence binding t
39	14.6	50.3	50	22 AAL30622	Sequence binding t
40	14.6	50.3	36	11 AAO04971	Oligonucleotide ta
41	14.6	50.3	36	14 AAO36224	Sequence binding t
42	14.6	50.3	37	11 AAO04970	Oligonucleotide ta
43	14.6	50.3	37	14 AAO36223	Sequence binding t
44	14.6	50.3	38	15 AAO79204	Guanosine rich oli
45	14.6	50.3	38	18 AAT51622	Viral integrase in

ALIGNMENTS

RESULT 1

AAC91745

27-MAR-2001 (first entry)

Thrombin-binding aptamer, ODN 2.

Thrombin-binding aptamer: exosite 2; heparin binding site;
blood clot; anticoagulant; in vivo imaging; diagnostic tool;
protein quantitation; in vivo half-life; ss.

Synthetic.

WO200078364-A2.

28-DEC-2000.

22-JUN-2000; 2000MO-CA00751.

22-JUN-1999; 99US-0139896.

(UVAL-) UNIV ALBERTA SIMON FRASER.

Dougan AH, Weitz JI;
WPI; 2001-091498/10.

Novel composition for inhibiting and preventing blood coagulation and
for imaging blood clots in vivo, comprises a nucleic acid that binds to

PT blood clot and complexed at its 5' or 3' end or both with a protein -
 XX
 PS Example 1; Page 5; 49pp; English.
 CC The invention relates to a composition comprising an aptamer which
 CC binds to a blood clot or to a protein component of a mammalian blood
 CC coagulation cascade, and a protein (other than the target protein)
 CC complexed with either or both the 5' and 3' ends of the aptamer. The
 CC proteins used in the composition can be covalently or non-covalently
 CC bound to the aptamer termini, and serve to extend the in vivo half-life
 CC of the aptamer. The aptamer/protein complexes of the invention are used
 CC to inhibit and prevent the coagulation of blood in a patient requiring
 CC anticoagulation treatment. Complexes may also be radiolabelled and used
 CC to image blood clots in vivo. The complexes can additionally be used to
 CC detect and quantitate the amount of a target protein in a sample to
 CC provide a diagnosis of a disease state that is correlated with the amount
 CC of protein in the sample. The present sequence represents an aptamer
 CC which binds to the heparin binding site (exosite 2) of human thrombin
 CC which was used in an exemplification of the invention.

Sequence 29 BP; 4 A; 4 C; 14 G; 7 T; 0 other;

Query Match 100.0%; Score 29; DB 22; Length 29;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 agtccgtgttaggcaggttgggtgact 29
 |||||||||||||||||||||||||||||
 Db 1 agtccgtgttaggcaggttgggtgact 29

RESULT 2

AAS16530
 ID AAS16530 standard; DNA; 37 BP.

AC AAS16530;

DT 14-FEB-2002 (first entry)

DE Thrombin specific, DT-aptamer.

KW DT-aptamer; L-selectin; alpha-thrombin; plasma; blood;

KM bronchial aspirate; sandwich assay; ss.

OS Synthetic.

XX

Key Location/Qualifiers
 1

/*tag= a /mod_base= g

/note= "Optionally fluorescein labelled, if position 1

is labelled, position 37 is not labelled"

1.8 /tag= b /bound_moiety= "nucleotides 37-30"

/note= "Forms a double stranded region with

nucleotides 37-30 of this sequence"

12.13 /tag= c

/note= "Forms a guanine quartet structure with bases

16.17 /tag= d

/note= "Forms a guanine quartet structure with bases

21.22 /tag= e

/note= "Forms a guanine quartet structure with bases

25.26 /tag= f

/note= "Forms a guanine quartet structure with bases

FT

FT

FT

FT

FT

FT

FT misc_binding 30..37 13-12, 16-17 and 22-21 of this sequence"

/*tag= g /bound_moiety= "nucleotides 8-1"

/note= "Forms a double stranded region with

nucleotides 8-1 of this sequence"

modified_base 37

/*tag= h /mod_base= c

/note= "Optionally fluorescein labelled, if position 37

is labelled, position 1 is not labelled"

W0200179562-A1.

25-OCT-2001.

18-APR-2001; 2001MO-US12614.

18-APR-2000; 2000US-198016P.

(GILE-) GILEAD SCI INC.

Lln Y, Heli J, Jayasena S;

WPI; 2002-017628/02.

Novel aptamer based two-site binding sandwich assay for detecting

target compounds such as thrombin and L-selectin in a biological fluid,

employs nucleic acid ligands as capture and/or reporter molecules

Example 1; Fig 1A; 47pp; English.

The invention describes a novel method of detecting the presence of a

target compound in a substance which may contain the target compound. The

method involves exposing the substance to a capture molecule (CM) capable

of binding to the target molecule (TM) and immobilised on a solid

support. A reporter molecule (RM) capable of binding to the target

molecule is added to the CM:TM complex to detect the CM:TM complex,

where CM and/or RM are a nucleic acid ligand to TM. The method is useful

for detecting a target molecule such as a protein, preferably thrombin or

L-selectin in a biological fluid including plasma, blood and serum. The

assays detect human alpha-thrombin in buffer as well as in biological

fluids. Detection of the target compound is useful for clinical diagnosis

of physiological conditions in both human and veterinary diagnostics. The

nucleic acid ligand-based sandwich assays, designed on two different

types of beads that can be readily analysed in flow cytometry, allow

multiplexed analysis of a mixture of target protein in a single tube.

This sequence is the alpha-thrombin specific DT-aptamer, the capture

molecule used to detect alpha-thrombin in a sample using the method

described in the invention.

Sequence 37 BP; 6 A; 6 C; 16 G; 9 T; 0 other;

Query Match 100.0%; Score 29; DB 24; Length 37;

Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 agtccgtgttaggcaggttgggtgact 29
 |||||||||||||||||||||||||||||
 Db 5 agtccgtgttaggcaggttgggtgact 33

RESULT 3

AAS16540
 ID AAS16540 standard; DNA; 37 BP.

AC AAS16540;

DT 14-FEB-2002 (first entry)

DE Thrombin specific, DT-DIMR-F aptamer.

XX

XX KM DR-DIMR-F aptamer; L-selectin; alpha-thrombin; plasma; blood;
XX KW bronchial aspirate; sandwich assay; ss.
XX
XX Synthetic.

XX FH Key location/Qualifiers
XX FT modified_base 37
XX FT /*tag-
XX FT /mod_base- c
XX FT /note= "Two copies of this sequence are joined at the 3'
XX FT end, by glycerol backbones, to a branching
XX FT phosphoramidite; the phosphoramidite is also
XX FT bound by a phosphodiester bond to a thymine
XX FT labelled with fluorescein"

XX PN WO200179562-A1.
XX PD
XX PP 25-OCT-2001.
XX PE 18-APR-2001; 2001WO-US12614.
XX PT 18-APR-2000; 2000US-198016P.
XX PS (GILE-) GILEAD SCI INC.
XX PA Lin Y, Heil J, Jayasena S;
XX PI WPI; 2002-017628/02.
XX PR Novel aptamer based two-site binding sandwich assay for detecting
XX PS target compounds such as thrombin and L-selectin in a biological fluid,
XX PS employs nucleic acid ligands as capture and/or reporter molecules -

XX PS Disclosure; Page 32; 47pp; English.

CC XX The invention describes a novel method of detecting the presence of a
CC target compound in a substance which may contain the target compound. The
CC method involves exposing the substance to a capture molecule (CM) capable
CC of binding to the target molecule (TM) and immobilised on a solid
CC support. A reporter molecule (RM) capable of binding to the target
CC molecule is added to the CM:TM complex to detect the CM:TM:RM complex,
CC where CM and/or RM are a nucleic acid ligand to TM. The method is useful
CC for detecting a target molecule such as a protein, preferably thrombin or
CC L-selectin in a biological fluid including plasma, blood and serum. The
CC assays detect human alpha-thrombin in buffer as well as in biological
CC fluids. Detection of the target compound is useful for clinical diagnosis
CC of physiological conditions in both human and veterinary diagnostics. The
CC nucleic acid ligand-based sandwich assays, designed on two different
CC types of beads that can be readily analysed in flow cytometry, allow
CC multiplexed analysis of a mixture of target protein in a single tube.
CC This sequence is the alpha-thrombin specific DR-DIMR-F aptamer, a
CC derivative of DR-aptamer AAS16530 consisting of two DR-aptamer joined to
CC a fluorescein labelled branching phosphoramidite, this forms the capture
CC molecule used to detect alpha-thrombin in a sample using the method
CC described in the invention.

XX CC Sequence 37 BP; 6 A; 6 C; 16 G; 9 T; 0 other;

OY Query Match 100.0%; Score 29; DB 24; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 agtcgctgtatagcgcaggttggagtact 29
|||||
db 5 agtccgtgtatagcgcaggttggagtact 33

RESULT 4
ID AAO98404 standard; RNA; 38 BP.
CC AAO98404;

```

XX 08-AUG-1996 (first entry)
XX Truncated SELEX derived DNA thrombin ligand 60-18(38).
XX
XX Family 1; family 2; ligand; thrombin;
XX systematic evolution of ligands by exponential enrichment; SELEX;
XX heparin; selection; region of homology; inhibitor; ss.
XX
XX Synthetic.
XX
XX MO5521853-A1.
XX
XX 17-AUG-1995.
XX
XX 06-FEB-1995; 95WO-US01458.
XX
XX 28-MAR-1994; 94US-0219012.
XX 10-FEB-1994; 94US-0195005.
XX 11-JUN-1990; 90US-0536428.
XX 10-JUN-1991; 91US-0714131.
XX 22-APR-1993; 93US-0061691.
XX
XX (NEXS-) NEXSTAR PHARM INC.
XX
XX Gold L, Janjic N, Tasset D;
XX
XX WPI: 1995-293073/38.
XX
XX Identification of ligands to basic fibroblast growth factor and
XX thrombin - which can be modified for increased in vivo stability
XX
XX Claim 39; Page 98; 236pp; English.
XX
XX The sequences given in AA098397-405 represent DNA ligands directed to
XX thrombin which were isolated using systematic evolution of ligands by
XX exponential enrichment (SELEX). Two populations of single stranded
XX (ss) DNA molecules with either 30N or 60N variable regions with 5' and
XX 3' flxed regions were synthesised. Thrombin and DNA were incubated in
XX a buffer at 37 deg.C for 5 mins. The thrombin-bound DNA is removed by
XX filtration. A double stranded product was created and amplified by PCR,
XX and a ssDNA template pool was isolated from this by alkaline
XX denaturation. This ssDNA template pool was used for the following round
XX of SELEX. Individual clones were isolated and the dissociation
XX constants (Kd) were determined. Kd's ranged from 0.4-9.4 nM for the 30N
XX DNA's and from 0.9-2.5 nM for the 60N DNA's. A truncated ligand given in
XX AA098404 was derived from the high affinity clone 60-18 and has a Kd of
XX 1.9 nM and inhibits clotting.
XX
XX Sequence 38 BP; 6 A; 6 C; 17 G; 9 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 29; DB 16; Length 38;
XX Best local Similarity 100.0%; Pred. NO. 0.014;
XX Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 agtcgctgagtagggcaggctggagtgact 29
XX ||||||||||||||||||||||||||||
XX 2 agtcgcgtgtagggcaggctggagtgact 30
XX
XX RESULT 5
XX AA086654
XX ID AA086654 standard; DNA; 38 BP.
XX
XX AA086654;
XX
XX 08-MAY-1998 (first entry)
XX
XX Spectroscopically detectable nucleic acid ligand compound #2.
XX
XX Spectroscopically detectable; detection; phosphorothioate;
XX fluorescein; thiazole orange; ss.
XX

```

```

XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1
FT /tag= a
FT /note= "Guaninel labeled with fluorescein via
FT a C6 linker molecule via a C3 linker"
XX
XX WO9622383-A1.
XX
XX 25-JUL-1996.
XX
XX 21-JUL-1995; 95WO-US09237.
XX
XX 20-JAN-1995; 95US-0376329.
XX
XX (BECT ) BECTON DICKINSON CO.
XX (NEXS-) NEXSTAR PHARM INC.
XX
XX Gold L, Malinowski DP, Pltner JB, Vonk GP;
XX WPI: 1996-354540/35.
XX
XX Detection of target cpds. such as thrombin - using spectroscopically
XX detectable nucleic acid ligands
XX
XX Claim 8; Figure 1; 37pp; English.
XX
XX This sequence represents a spectroscopically detectable nucleic acid
XX ligand which was used to detect the presence or absence of a target
XX compound (thrombin) in a sample. This ligand can also be used for
XX monitoring the binding of target compounds (such as growth factors) to
XX their receptors in competition-based assays. It is thus useful in
XX diagnostic assays. Spectroscopically detectable nucleic acid
XX ligands of the invention may be used to detect e.g. thrombin, elastase,
XX cell surface markers, growth factors, growth factor receptors, whole
XX cells or viral particles present in biological samples such as blood.
XX The receptor molecules are typically relatively small in relation to
XX traditional receptor molecules such as antibodies. Any additional weight
XX or volume added to the receptor molecules (even in the form of a small
XX target) will significantly increase the weight or volume of the
XX labelled receptor molecule and therefore permit detection of the
XX relatively significant energy differences involved (between bound and
XX unbound labelled receptor molecules).
XX
XX Sequence 38 BP; 6 A; 6 C; 17 G; 9 T; 0 other:
SQ
XX
XX Query Match 100.0%; Score 29; DB 17; Length 38;
XX Best Local Similarity 100.0%; Pred. No. 0.014;
XX Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 agtcctgtgtagggcaggttggtgact 29
DB 2 agtcctgtgtagggcaggttggtgact 30
XX
XX
XX RESULT 6
XX AAT38802
XX ID AAT38802 standard; DNA; 38 BP.
XX
XX AAT38802:
XX
XX 26-SEP-1997 (first entry)
XX
XX Thrombin ligand for use in therapeutic or diagnostic complex.
XX
XX Therapy; diagnosis; complex; ligand; lipophilic compound;
XX non-immunogenic; high molecular weight compound; SELRX; PEG;
XX targeted delivery; liposome; dextran; albumin; magnetic;
XX systematic evolution of ligands by exponential enrichment;
XX polyethylene glycol; cholesterol; dialkyl; diacyl; glycerol;

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```

XX thrombin; ss.
XX
XX Synthetic.
OS
XX
XX WO9634876-A1.
XX
XX 07-NOV-1996.
XX
XX 02-MAY-1996; 96WO-US06171.
XX
XX 05-JUN-1995; 95US-0464443.
XX 04-MAY-1995; 95US-0434465.
XX
XX (NEXS-) NEXSTAR PHARM INC.
XX
XX Gold L, Janjic N, Schmidt PG;
XX WPI: 1996-506093/50.
XX
XX Compsn. contg. nucleic acid ligand and lipophilic or high mol.wt.
XX non-immunogenic cpd. - for diagnosis or therapy, has better
XX pharmaco:kinetics, intracellular uptake and/or targeting than free
XX ligand
XX
XX Example 2; Fig 1A; 107pp; English.
XX
XX A novel therapeutic or diagnostic complex comprises a nucleic acid
XX ligand, i.e. the present sequence, and a lipophilic compound or a
XX non-immunogenic, high molecular weight compound. The complex can be
XX used for the targeted delivery of any therapeutic or diagnostic
XX agent, e.g. fungicide, anti-tumour agent or another nucleic acid
XX ligand, e.g. one that blocks the mutated form of p21. A ligand on
XX the surface of the complex may also target circulating proteins,
XX e.g. auto-antibodies, for removal by the reticulo-endothelial
XX system, for autoimmune disease treatment. When the high molecular
XX weight compound is magnetic, the complex can also be used for
XX nuclear magnetic resonance imaging. Compared to the ligand alone,
XX the complex has better pharmacokinetic properties, cellular uptake
XX and/or targeting properties. Many ligands can be included in the
XX same composition, allowing multiple binding interactions at the
XX target.
XX
XX Sequence 38 BP; 6 A; 6 C; 17 G; 9 T; 0 other:
SQ
XX
XX Query Match 100.0%; Score 29; DB 17; Length 38;
XX Best Local Similarity 100.0%; Pred. No. 0.014;
XX Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 agtcctgtgtagggcaggttggtgact 29
DB 2 agtcctgtgtagggcaggttggtgact 30
XX
XX
XX RESULT 7
XX AAT85812
XX ID AAT85812 standard; DNA; 38 BP.
XX
XX AAT85812:
XX
XX 17-NOV-1997 (first entry)
XX
XX Thrombin-binding nucleic acid ligand.
XX
XX Thiazole orange; fluorescein; spectroscopic assay;
XX fluorescence polarisation detection; thrombin; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1
FT /tag= a
FT /note= "5'-labelled with fluorescein via a C6

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```

FT      linker arm (= Compound 2)
XX      US5650275-A.
PN      22-JUL-1997.
XX      18-JUL-1994; 94US-0276271.
XX      18-MAY-1995; 95US-0443957.
XX      11-JUN-1990; 90US-0536428.
XX      10-JUN-1991; 91US-0714131.
XX      17-AUG-1992; 92US-0931473.
XX      07-OCT-1993; 93US-0134028.
XX      28-APR-1994; 94US-0234997.
XX      18-JUL-1994; 94US-0276271.
XX      (GOLD/) GOLD L.
XX      (MALI/) MALINOWSKI D P.
XX      (PITN/) PITNER J B.
XX      (VONK/) VONK G P.
PA      Gold L, Malinowski DP, Pitner JB, Vonk GP;
DR      WPI: 1997-384664/35.
XX      Determining the presence of target compounds such as thrombin or
XX      elastase - using spectroscopically detectable labelled nucleic acid
XX      ligands and measurement of spectroscopic emissions.
XX      Claim 7; Column 8; 14pp; English.
XX      Spectroscopically detectable labelled nucleic acid ligands are used
XX      in a claimed method for determining the presence of a target compound
XX      in a sample. An increase in the spectroscopic emission of the
XX      ligand in the presence of a sample relative to the ligand alone is
XX      indicative of the presence of the target compound in the sample.
XX      Target molecules may be proteins, peptides, cell surface markers,
XX      carbohydrates, polysaccharides, glycoproteins, hormones, receptors,
XX      antibodies, antibodies, co-factors, inhibitors, drugs, dyes, nutrients,
XX      growth factors, amino acids, ATP, whole cells or viral particles.
XX      The present sequence is a preferred nucleic acid ligand for
XX      detecting thrombin. When labelled with fluorescein it is designated
XX      Compound 2.
XX      Sequence 38 BP; 6 A; 6 C; 17 G; 9 T; 0 other:
SQ
Query Match      100.0%; Score 29; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. NO. 0.014;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 agtcgctgtaggcaaggttgaggtagct 29
        |||||||||||||||||||||||||||
        2 agtcgctgtaggcaaggttgaggtagct 30
DB
RESULT 8
AAT80049
ID      AAT80049 standard; DNA: 38 BP.
XX
AC      AAT80049;
XX
DT      04-NOV-1997 (first entry)
XX
DE      Thrombin binding ligand #2.
XX
KW      Thrombin; binding ligand; cell surface marker; hormone; receptor; human;
KW      antibody; theophylline; viral particle; environmental discharge;
KW      elastase; liquid waste; growth factor; chorionic gonadotropin; ss.
XX
OS      Synthetic.
XX
FH      Key      Location/Qualifiers

```

```

FT      misc-feature      1
XX      US5641629-A.      /tag= a
XX      24-JUN-1997.      /note= "fluorescein labelled"
XX      11-JUN-1990; 90US-0536428.
XX      18-MAY-1995; 95US-0443957.
XX      11-JUN-1990; 90US-0536428.
XX      10-JUN-1991; 91US-0714131.
XX      17-AUG-1992; 92US-0931473.
XX      07-OCT-1993; 93US-0134028.
XX      28-APR-1994; 94US-0234997.
XX      18-JUL-1994; 94US-0276271.
XX      20-JAN-1995; 95US-0376329.
XX      (GOLD/) GOLD L.
XX      (MALI/) MALINOWSKI D P.
XX      (PITN/) PITNER J B.
XX      (VONK/) VONK G P.
PA      Gold L, Malinowski DP, Pitner JB, Vonk GP;
DR      WPI: 1997-34038/31.
XX      Determining presence or absence of target compounds such as thrombin
XX      or elastase - using spectroscopically detectable labelled nucleic
XX      acid ligands and measurement of fluorescence polarisation,
XX      anisotropy values or rotation correlation times.
XX      Example 1; Column 8; 15pp; English.
XX      AAT80048-180050 represent thrombin binding ligands. These sequences can
XX      be labelled and used as the spectroscopically detectable labelled
XX      nucleic acid ligands (SDNAL) in the method of the invention. The method
XX      of the invention is to detect the presence or absence of a target
XX      compound (TC) in a sample. The TC for detection, include proteins, cell
XX      surface markers, polysaccharides, hormones, receptors, antibodies, drugs,
XX      dyes, ATP, theophylline, whole cells and viral particles. The method
XX      comprises measuring at least one of the fluorescence polarisation,
XX      anisotropy values or rotational correlation times of a SDNAL to the TC. It
XX      then adding to the sample the SDNAL so that the SDNAL binds to the TC. It
XX      is then determined whether there is a difference between at least one of
XX      the fluorescence polarisation, anisotropy values or rotation correlation
XX      times of the mixture of SDNAL bound to the TC and sample, and the SDNAL
XX      alone. An increase in at least one of these values in the mixture
XX      relative to the SDNAL alone is indicative of the presence of the TC in
XX      the sample. The SDNAL allows quantitative and qualitative determination
XX      of differences in detectable emissions to determine the presence or
XX      absence of specific target molecules in samples. The method may be used
XX      for assays of target ligands in biological materials, foods or
XX      environmental discharges (such as liquid wastes). The target is
XX      especially thrombin, elastase, a cell surface marker, a growth factor,
XX      human chorionic gonadotropin, a whole cell or a viral particle.
XX      Sequence 38 BP; 6 A; 6 C; 17 G; 9 T; 0 other:
SQ
Query Match      100.0%; Score 29; DB 18; Length 38;
Best Local Similarity 100.0%; Pred. NO. 0.014;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 agtcgctgtaggcaaggttgaggtagct 29
        |||||||||||||||||||||||||||
        2 agtcgctgtaggcaaggttgaggtagct 30
DB
RESULT 9
AAF70817
ID      AAF70817 standard; DNA: 38 BP.

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```

XX AC AAF70817;
XX AC 20-APR-2001 (first entry)
XX DT Thrombin high affinity ligand #64.
XX DE
XX KW Ligand; basic fibroblast growth factor; bFGF; gene therapy; vascular;
XX KM atherosclerosis; angioplasty; stability; ss.
XX OS unidentified.
XX OS US6177557-B1.
XX PN 23-JAN-2001.
XX PD
XX PE 05-AUG-1996; 96US-0687421.
XX PR 11-JUN-1990; 90US-0536428.
XX PR 10-JUN-1991; 91US-0714131.
XX PR 06-NOV-1992; 92US-0973333.
XX PR 10-FEB-1994; 94US-0195005.
XX PR 28-MAR-1994; 94US-0219012.
XX PA (NEXS-) NEXSTAR PHARM INC.
XX PI Janjic N, Gold L, Tasset D;
XX PT WPI; 2001-158583/16.
XX DR
XX PT Novel nucleic acid ligands to basic fibroblast growth factor that are
XX PT useful as inhibitors of basic fibroblast growth factors and 2'-amino
XX PT modified RNA ligands, exhibit increased in vivo stability.
XX PS Example 19; Column 61-62; 153pp; English.
XX XX
XX CC The present invention relates to a purified and isolated non-naturally
XX CC occurring DNA ligands to basic fibroblast growth factor (bFGF).
XX CC The ligands are useful as part of gene therapy treatments and
XX CC for diagnosing pathogenesis of vascular diseases including
XX CC initiation and progression of atherosclerosis, acute coronary
XX CC syndromes, vein graft disease and restenosis following coronary
XX CC angioplasty. The ligands have improved stability in vivo.
XX CC
XX SO Sequence 38 BP; 6 A; 6 C; 17 G; 9 T; 0 other;

Query Match          100.0%; Score 29; DB 22; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agtcgctgtaggtaggcaggttggtgact 29
   |||
Db 2 agtcgctgtaggtaggcaggttggtgact 30

RESULT 10
AA87088
ID AAX87088 standard; DNA; 39 BP.
XX
XX AAX87088;
XX
XX 20-SEP-1999 (first entry)
XX
XX DNA ligand T39 to human thrombin.
XX
XX Platelet derived growth factor; PDGF; human; ligand; SELEX;
XX KW systematic evolution of ligands by exponential enrichment;
XX KM single stranded DNA; ssDNA; angiogenesis; restenosis; tumour;
XX KM cancer; fibrosis; therapy; thrombin; ss.
XX
XX OS Synthetic.
XX

```

```

PH Key Location/Qualifiers
FT modified_base 39
FT FT /*tag= a
FT FT /mod_base= OTHER
FT FT /note= "inverted orientation (3'-3'-linked),
FT FT reduces 3'-exonuclease degradation"

XX PN WO931119-A1.
XX PD
XX PD 24-JUN-1999.
XX
XX 29-APR-1998; 98WO-US09050.
XX
XX 16-DEC-1997; 97US-0991743.
XX
XX (NEXS-) NEXSTAR PHARM INC.
XX PA Gold L, Janjic N;
XX PI
XX DR WPI; 1999-405022/34.
XX
XX PT Complex comprises a platelet derived growth factor nucleic acid
XX PT ligand
XX
XX PS Example 3; Page 52; 156pp; English.
XX XX
XX CC This sequence represents DNA ligand T39 to human thrombin. It was
XX CC used as a control in experiments designed to examining binding of
XX CC minimal DNA ligands (see AAX87083-85) to human platelet derived
XX CC growth factor (PDGF). The invention discloses a method for
XX CC preparing a complex of a PDGF nucleic acid ligand and a
XX CC non-immunogenic high mol.wt. compound (e.g. PEG) or lipophilic
XX CC compound (e.g. a glycerol lipid). Such complexes are used as
XX CC inhibitors of PDGF mediated angiogenesis, to inhibit the growth of
XX CC tumours, to inhibit fibrosis (especially kidney, lung, bone marrow
XX CC or radiation treatment associated fibrosis) or to inhibit
XX CC restenosis, especially in-stent restenosis or restenosis in a
XX CC coronary artery or non-coronary vessel. They can also be used to
XX CC target a therapeutic or diagnostic agent to a biological target
XX CC expressing PDGF.
XX CC
XX SO Sequence 39 BP; 6 A; 6 C; 17 G; 10 T; 0 other;

Query Match          100.0%; Score 29; DB 20; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agtcgctgtaggtaggcaggttggtgact 29
   |||
Db 2 agtcgctgtaggtaggcaggttggtgact 30

RESULT 11
AAS16539
ID AAS16539 standard; DNA; 42 BP.
XX
XX AAS16539;
XX
XX 14-FEB-2002 (first entry)
XX
XX Thrombin specific; DT-5'-LNK-aptamer.
XX
XX DT-5'-LNK-aptamer; L-selectin; alpha-thrombin; plasma; blood;
XX KW bronchial aspirate; sandwich assay; ss.
XX
XX OS Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1
FT FT /*tag= a
FT FT /mod_base= t
FT FT /label= Fluorescein

```

FT	misc_feature	1..5	
FT	/tag-	b	
FT	/label	"Thymine-linker	
FT	/function-	"Alleviates steric crowding between aptamers on the surface of the captured particle"	
FT			
PT	misc_binding	6..13	
PT	/tag-	c	
FT	/bound_moiety-	"nucleotides 42-35"	
FT	/note-	"Forms a double stranded region with nucleotides 42-35 of this sequence"	
FT			
PT	misc_structure	17..18	
PT	/tag-	d	
FT	/note-	"Forms a guanine quartet structure with bases 22-21, 26-27 and 31-30 of this sequence"	
FT			
PT	misc_structure	21..22	
PT	/tag-	e	
FT	/note-	"Forms a guanine quartet structure with bases 18-17, 27-26 and 30-31 of this sequence"	
FT			
PT	misc_structure	26..27	
PT	/tag-	f	
FT	/note-	"Forms a guanine quartet structure with bases 17-18, 22-21 and 31-30 of this sequence"	
FT			
PT	misc_structure	30..31	
PT	/tag-	g	
FT	/note-	"Forms a guanine quartet structure with bases 18-17, 21-22 and 27-26 of this sequence"	
FT			
PT	misc_binding	35..42	
PT	/tag-	h	
FT	/bound_moiety-	"nucleotides 13-6"	
FT	/note-	"Forms a double stranded region with nucleotides 13-6 of this sequence"	
XX			
PN	WO200179562-A1.		
XX			
PD	25-OCT-2001.		
XX			
XX	18-APR-2001; 2001W0-US12614.		
XX			
PR	18-APR-2000; 2000US-198016P.		
XX	(GILE-) GILEAD SCI INC.		
PA	Lin Y, Heil J, Jayasena S;		
PI			
DR	WPI; 2002-017628/02.		
XX			
PT	Novel aptamer based two-site binding sandwich assay for detecting target compounds such as thrombin and L-selectin in a biological fluid, employs nucleic acid ligands as capture and/or reporter molecules -		
XX			
PT	Disclosure; Page 32; 47pp; English.		
XX			
CC	The invention describes a novel method of detecting the presence of a target compound in a substance which may contain the target compound. The method involves exposing the substance to a capture molecule (CM) capable of binding to the target molecule (TM) and immobilised on a solid support. A reporter molecule (RM) capable of binding to the target molecule is added to the CM:TM complex to detect the CM:TM:RM complex, where CM and/or RM are a nucleic acid ligand to TM. The method is useful for detecting a target molecule such as a protein, preferably thrombin or L-selectin in a biological fluid including plasma, blood and serum. The assays detect human alpha-thrombin in buffer as well as in biological fluids. Detection of the target compound is useful for clinical diagnosis of physiological conditions in both human and veterinary diagnostics. The nucleic acid ligand-based sandwich assays, designed on two different types of beads that can be readily analysed in flow cytometry, allow multiplexed analysis of a mixture of target protein in a single tube. This sequence is the alpha-thrombin specific DT-5'-LNK-aptamer, a derivative of the DT-aptamer (AS16530) the capture molecule used to detect alpha-thrombin in a sample using the method described in the invention.		
CC			
CC			
CC			
CC			
CC			
CC			
CC			
XX	Sequence 42 BP; 6 A; 6 C; 16 G; 14 T; 0 other;		
XX			

Query Match	100.0%	Score 29	DB 24	Length 42
Best Local Similarity	100.0%	Pred. No. 0.014		
Matches 29	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Oy	1	agtcctgtaggcagattgaggtgact 29		
Db	10	agtcctgtaggcaggttgggtgact 38		
RESULT 12				
AA516537				
AA516537	standard	DNA: 43 BP.		
AC	AA516537:			
DT	14-FEB-2002	(first entry)		
XX				
DE	Thrombin specific, DT-3'-LNK-aplamer.			
XX				
KN	DT-3'-LNK-aplamer: l-selectin; alpha-Thrombin; plasma; blood;			
XX	bronchial aspirate; sandwich assay; ss.			
OS	Synthetic.			
XX				
FH	Key	Location/Qualifiers		
FT	misc_binding	1..8		
FT		/*tag= a		
FT		/bound_moiety= "nucleotides 37-30"		
FT		/note= "Forms a double stranded region with nucleotides 37-30 of this sequence"		
FT	misc_structure	12..13		
FT		/*tag= b		
FT		/note= "Forms a guanine quartet structure with bases 17-16, 21-22 and 26-25 of this sequence"		
FT	misc_structure	16..17		
FT		/*tag= c		
FT		/note= "Forms a guanine quartet structure with bases 13-12, 22-21 and 25-26 of this sequence"		
FT	misc_structure	21..22		
FT		/*tag= d		
FT		/note= "Forms a guanine quartet structure with bases 12-13, 17-16 and 26-25 of this sequence"		
FT	misc_structure	25..26		
FT		/*tag= e		
FT		/note= "Forms a guanine quartet structure with bases 13-12, 16-17 and 22-21 of this sequence"		
FT	misc_binding	30..37		
FT		/*tag= f		
FT		/bound_moiety= "nucleotides 8-1"		
FT		/note= "Forms a double stranded region with nucleotides 8-1 of this sequence"		
FT	misc_feature	38..43		
FT		/*tag= g		
FT		/label= "Thymine linker		
FT		/function= "Alleviates steric crowding between aptamers on the surface of the captured particle"		
FT	modified_base	43		
FT		/*tag= h		
FT		/mod_base= t		
FT		/label= "Fluorescein		
PN	W0200179562-A1.			
XX				
PD	25-OCT-2001.			
XX				
PF	18-APR-2001; 2001WO-US12614.			
XX				
PR	18-APR-2000; 2000US-198016P.			
XX				
PA	(GILE-) GILEAD SCI INC.			
XX				

PI Lin Y, Heil J, Jayasena S;
 XX WPI; 2002-017628/02.
 DR
 XX Novel aptamer based two-site binding sandwich assay for detecting
 PT target compounds such as thrombin and L-selectin in a biological fluid.
 PT employs nucleic acid ligands as capture and/or reporter molecules
 PS
 XX Disclosure; Page 32; 47pp; English.
 XX
 CC The invention describes a novel method of detecting the presence of a
 CC target compound in a substance which may contain the target compound. The
 CC method involves exposing the substance to a capture molecule (CM) capable
 CC of binding to the target molecule (TM) and immobilised on a solid
 CC support. A reporter molecule (RM) capable of binding to the target
 CC molecule is added to the CM:TM complex to detect the CM:TM complex,
 CC where CM and/or RM are a nucleic acid ligand to TM. The method is useful
 CC for detecting a target molecule such as a protein, preferably thrombin or
 CC L-selectin in a biological fluid including plasma, blood and serum. The
 CC assays detect human alpha-thrombin in buffer as well as in biological
 CC fluids. Detection of the target compound is useful for clinical diagnosis
 CC of physiological conditions in both human and veterinary diagnostics. The
 CC nucleic acid ligand-based sandwich assays, designed on two different
 CC types of beads that can be readily analysed in flow cytometry, allow
 CC multiplexed analysis of a mixture of target protein in a single tube.
 CC This sequence is the alpha-thrombin specific DT-3'-LNA-aptamer, a
 CC derivative of the DT-aptamer (AAS16530) the capture molecule used to
 CC detect alpha-thrombin in a sample using the method described in the
 CC invention.
 CC
 XX Sequence 43 BP; 6 A; 6 C; 16 G; 15 T; 0 other;
 SO

Query Match 100.0%; Score 29; DB 24; Length 43;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 agtcggtgtaggcaggttggtggtact 29
 ||||||||||||||||||||||||||||
 DB 5 agtcggtgtaggcaggttggtggtact 33

RESULT 13
 AAT00205
 ID AAT00205 standard; DNA; 30 BP.
 XX
 AC AAT00205;
 AC

14-AUG-1996 (first entry)
 DE Thrombin DNA ligand, clone #6.
 XX
 KW Family 1; family 2; ligand; thrombin;
 KW systematic evolution of ligands by exponential enrichment; SELEX;
 KW heparin; selection; region of homology; inhibitor; ss.
 OS
 XX Synthetic.
 XX
 PN WC9521853-A1.
 XX
 PD 17-AUG-1995.
 XX
 PF 06-FEB-1995; 95WO-US01458.
 XX
 PR 28-MAR-1994; 94US-0219012.
 PR 10-FEB-1994; 94US-0195005.
 PR 11-JUN-1990; 90US-0536428.
 PR 10-JUN-1991; 91US-0714131.
 PR 22-APR-1993; 93US-0061691.
 PR
 XX (NEXS-) NEXSTAR PHARM INC.
 PA
 XX Gold L, Janjic N, Tasset D;
 PI

XX
 DR WPI; 1995-293073/38.
 XX
 PT Identification of ligands to basic fibroblast growth factor and
 PT thrombin - which can be modified for increased in vivo stability
 XX
 PS Claim 39; Page 95; 236pp; English.
 XX
 CC The sequences given in AAT00202-25 and AAT00227-57 represent two groups
 CC of ligands to thrombin. These sequences were isolated using the single
 CC stranded DNA molecules given in AAT00201 and AAT00226 which comprise a
 CC 30N and a 60N variable region, respectively. These ligands were
 CC isolated using systematic evolution of ligands by exponential enrichment
 CC (SELEX). The selection was conducted in a buffer solution at 37 deg. C.
 CC After 12 rounds of selection, no additional improvement in binding was
 CC seen. By studying regions of homology between the isolated ligands, a
 CC truncated ligand of 38 nucleotides (see AA098403-04) was identified which
 CC retains high affinity binding and inhibits clotting. These ligands are
 CC inhibitors of thrombin and are therefore useful in treating thrombin
 CC mediated conditions and in studying the structure and binding of
 CC thrombin.
 CC
 XX Sequence 30 BP; 5 A; 5 C; 14 G; 6 T; 0 other;
 SO

Query Match 68.3%; Score 19.8; DB 16; Length 30;
 Best Local Similarity 91.3%; Pred. No. 61;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 ccgtgtaggcaggttggtggtg 26
 ||||||||||||| |||||
 DB 5 ccgtgtaggcaggttggtggtg 27

RESULT 14
 AAF70757
 ID AAF70757 standard; DNA; 30 BP.
 XX
 AC AAF70757;
 AC

20-APR-2001 (first entry)
 DE Thrombin high affinity ligand #4.
 XX
 KW Ligand; basic fibroblast growth factor; bFGF; gene therapy; vascular;
 KW atherosclerosis; angioplasty; stability; ss.
 OS
 XX Unidentified.
 XX
 PN US6177557-B1.
 XX
 PD 23-JAN-2001.
 XX
 PF 05-AUG-1996; 96US-0687421.
 XX
 PR 11-JUN-1990; 90US-0536428.
 PR 10-JUN-1991; 91US-0714131.
 PR 06-NOV-1992; 92US-0973333.
 PR 10-FEB-1994; 94US-0195005.
 PR 28-MAR-1994; 94US-0219012.
 PR
 XX (NEXS-) NEXSTAR PHARM INC.
 PA
 XX Janjic N, Gold L, Tasset D;
 PI
 DR WPI; 2001-158583/16.
 XX
 PT Novel nucleic acid ligands to basic fibroblast growth factor that are
 PT useful as inhibitors of basic fibroblast growth factors and 2'-amino
 PT modified RNA ligands, exhibit increased in vivo stability
 XX
 PS Example 19; Column 57-58; 153pp; English.
 XX

CC The present invention relates to a purified and isolated non-naturally
 CC occurring DNA ligands to basic fibroblast growth factor (bFGF).
 CC The ligands are useful as part of gene therapy treatments and
 CC for diagnosing pathogenesis of vascular diseases including
 CC initiation and progression of atherosclerosis, acute coronary
 CC syndromes, vein graft disease and restenosis following coronary
 CC angioplasty. The ligands have improved stability in vivo.
 XX
 SQ Sequence 30 BP; 5 A; 5 C; 14 G; 6 T; 0 other;

Query Match 68.3%; Score 19.8; DB 22; Length 30;
 Best Local Similarity 91.3%; Pred. No. 61;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 ccgtgtagggcagggttgagg 26
 |||||
 Db 5 ccgtgtagggcagggttgagg 27

RESULT 15
 00218
 AAT00218 standard; DNA: 30 BP.

XX AAT00218;
 AC
 XX 14-AUG-1996 (first entry)
 DT
 XX
 DE Thrombin DNA ligand, clone #26.
 XX
 KW Family 1; family 2; ligand; thrombin;
 KW systematic evolution of ligands by exponential enrichment; SELEX;
 KW heparin; selection; region of homology; inhibitor; ss.
 XX
 OS Synthetic.
 OS
 XX W09521853-A1.
 PN
 XX 17-AUG-1995.
 PD
 XX
 XX 06-FEB-1995; 95MO-US01458.
 PF
 XX 28-MAR-1994; 94US-0219012.
 PR 10-FEB-1994; 94US-0195005.
 PR 11-JUN-1990; 90US-0536428.
 PR 10-JUN-1991; 91US-0714131.
 PR 22-APR-1993; 93US-0061691.
 XX
 (NEXS-) NEXSTAR PHARM INC.

XX Gold L, Janjic N, Tasset D;
 DR WPI: 1995-293073/38.
 XX

PT Identification of ligands to basic fibroblast growth factor and
 XX thrombin - which can be modified for increased in vivo stability
 XX
 PS Claim 39; Page 95; 236pp; English.
 XX

CC The sequences given in AAT00207-25 and AAT00227-57 represent two groups
 CC of ligands to thrombin. These sequences were isolated using the single
 CC stranded DNA molecules given in AAT00201 and AAT00226 which comprise a
 CC 30N and a 60N variable region, respectively. These ligands were
 CC isolated using systematic evolution of ligands by exponential enrichment
 CC (SELEX). The selection was conducted in a buffer solution at 37 deg. C.
 CC After 12 rounds of selection, no additional improvement in binding was
 CC seen. By studying regions of homology between the isolated ligands, a
 CC truncated ligand of 38 nucleotides (see AAQ98403-04) was identified which
 CC retains high affinity binding and inhibits clotting. These ligands are
 CC inhibitors of thrombin and are therefore useful in treating thrombin
 CC mediated conditions and in studying the structure and binding of
 CC thrombin.
 XX

SQ Sequence 30 BP; 4 A; 3 C; 14 G; 9 T; 0 other;

Query Match 66.9%; Score 19.4; DB 16; Length 30;
 Best Local Similarity 95.2%; Pred. No. 88;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 cgtgtagggcagggttgagg 25
 |||||
 Db 9 cgtgtagggcagggttgagg 29

Search completed: June 6, 2002, 16:08:48
 Job time: 2149 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 6, 2002, 16:04:32 : Search time 51.8 Seconds
(without alignments)
137.517 Million cell updates/sec

Title: US-09-599-220-2

Perfect score: 29
Sequence: 1 aglcqglgtaagcaggtg99gtact 29

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 543772

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/lna/5A.COMB.seq:*
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3: /cgn2_6/ptodata/2/lna/6A.COMB.seq:*
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5: /cgn2_6/ptodata/2/lna/PCITUS.COMB.seq:*
6: /cgn2_6/ptodata/2/lna/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	36	3 US-08-434-465-3	Sequence 3, Appl
2	29	100.0	38	1 US-08-219-012-91	Sequence 91, Appl
3	29	100.0	38	1 US-08-376-329-2	Sequence 2, Appl
4	29	100.0	38	1 US-08-276-271-2	Sequence 2, Appl
5	29	100.0	38	3 US-08-434-465-6	Sequence 6, Appl
6	29	100.0	38	4 US-08-687-421-279	Sequence 279, App
7	29	100.0	38	5 PCT-US95-09237-2	Sequence 2, Appl
8	29	100.0	39	1 US-08-479-7834-90	Sequence 90, Appl
9	29	100.0	39	1 US-08-479-725-90	Sequence 88, Appl
10	29	100.0	39	1 US-08-618-693-88	Sequence 88, Appl
11	29	100.0	39	4 US-08-973-124-177	Sequence 177, App
12	29	100.0	39	4 US-08-991-743C-88	Sequence 88, Appl
13	29	100.0	39	5 PCT-US96-08014-177	Sequence 177, App
14	29	100.0	40	3 US-08-434-465-9	Sequence 9, Appl
15	29	100.0	40	3 US-08-434-465-13	Sequence 13, Appl
16	29	100.0	41	3 US-08-434-465-17	Sequence 7, Appl
17	29	100.0	41	3 US-08-434-465-12	Sequence 12, Appl
18	29	100.0	41	3 US-08-434-465-15	Sequence 15, Appl
19	29	100.0	42	3 US-08-434-465-5	Sequence 5, Appl
20	29	100.0	42	3 US-08-434-465-8	Sequence 8, Appl
21	19.8	68.3	30	4 US-08-219-012-31	Sequence 31, Appl
22	19.8	68.3	30	4 US-08-687-421-219	Sequence 219, App
23	19.4	66.9	30	4 US-08-219-012-44	Sequence 44, Appl
24	19.4	66.9	30	4 US-08-687-421-232	Sequence 232, App
25	19	65.5	30	1 US-08-219-012-47	Sequence 47, Appl
26	19	65.5	30	4 US-08-687-421-235	Sequence 235, App
27	18.8	64.8	30	1 US-08-219-012-29	Sequence 29, Appl

ALIGNMENTS

28	18.8	64.8	30	4	US-08-687-421-217	Sequence 217, App
29	17.2	59.3	30	1	US-08-219-012-35	Sequence 35, Appl
30	17.2	59.3	30	4	US-08-687-421-223	Sequence 223, Appl
31	16	55.2	30	1	US-08-219-012-43	Sequence 43, Appl
32	16	55.2	30	4	US-08-687-421-231	Sequence 231, App
33	15.8	54.5	30	1	US-08-219-012-32	Sequence 32, App
34	15.8	54.5	30	4	US-08-687-421-220	Sequence 220, App
35	14.8	51.0	29	1	US-08-058-907-3	Sequence 3, Appl
36	14.8	51.0	30	1	US-07-786-902-7	Sequence 7, Appl
37	14.6	50.3	21	2	US-08-981-663-4	Sequence 4, Appl
38	14.6	50.3	25	2	US-08-981-663-64	Sequence 64, Appl
39	14.6	50.3	38	3	US-08-145-704-4	Sequence 4, Appl
40	14.6	50.3	38	3	US-08-987-574-4	Sequence 4, Appl
41	14.6	50.3	38	4	US-08-535-168-4	Sequence 4, Appl
42	14.6	50.3	38	4	US-09-017-974-4	Sequence 4, Appl
43	14.6	50.3	38	4	US-09-429-130-4	Sequence 4, Appl
44	14.6	50.3	38	5	PCT-US96-11786-4	Sequence 4, Appl
45	14.2	49.0	21	1	US-08-484-192-78	Sequence 78, Appl

RESULT 1
US-08-434-465-3
; Sequence 3, Application US/08434465
; Patent No. 6011020
; GENERAL INFORMATION:
; APPLICANT: LARRY GOLD, PAUL G. SCHMIDT, NEBOUSA JANJIC
; TITLE OF INVENTION: NUCLEIC ACID LIGAND COMPLEXES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson and Bratschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,465
; FILING DATE: 4-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/234,997
; FILING DATE: 28-APRIL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Diane H. McClearn
; REGISTRATION NUMBER: 33,960
; REFERENCE/DOCKET NUMBER: NEX29
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-434-465-3

Query Match 100.0%; Score 29; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 agtccgtgttagggcaggttggtgact 29
|||||
DB 2 agtccgtgttagggcaggttggtgact 30

RESULT 2
US-08-219-012-91
; Sequence 91, Application US/08219012
; Patent No. 5543293
; GENERAL INFORMATION:
; APPLICANT: Larry Gold
; APPLICANT: Diane Tasset
; TITLE OF INVENTION: Ligands of Thrombin
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beaton & Swanson, P.C.
; STREET: 4582 South Ulster Street Parkway, Suite #
; STREET: 403
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80237
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/219,012
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: none
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 850-9900
; TELEFAX: (303) 850-9401
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
08-219-012-91

Query Match 100.0%; Score 29; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 agtccgtgttagggcaggttggtgact 29
|||||
DB 2 agtccgtgttagggcaggttggtgact 30

RESULT 3
US-08-376-329-2
; Sequence 2, Application US/08376329
; Patent No. 5641629
; GENERAL INFORMATION:
; APPLICANT: Pltner, James B
; APPLICANT: Malinowski, Douglas P
; APPLICANT: Vonk, Glenn P
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: Spectroscopically Detectable Nucleic
; ACID LIGANDS
; NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard J. Roderick, Becton Dickinson and
; ADDRESSEE: Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: NJ
; COUNTRY: USA
; ZIP: 07417-1880
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/376,329
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hight, David W
; REGISTRATION NUMBER: 30,265
; REFERENCE/DOCKET NUMBER: P-3126
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 847 5317
; TELEFAX: 201 848 9228
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-376-329-2

Query Match 100.0%; Score 29; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 agtccgtgttagggcaggttggtgact 29
|||||
DB 2 agtccgtgttagggcaggttggtgact 30

RESULT 4
US-08-276-271-2
; Sequence 2, Application US/08276271
; Patent No. 5650275
; GENERAL INFORMATION:
; APPLICANT: Pltner, James B
; APPLICANT: Malinowski, Douglas P
; APPLICANT: Vonk, Glenn P
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: Spectroscopically Detectable Nucleic
; ACID LIGANDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard J. Roderick, Becton Dickinson and
; ADDRESSEE: Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: NJ
; COUNTRY: USA
; ZIP: 07417-1880
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,271
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:

NAME: Hiphel, David W
REGISTRATION NUMBER: 30,265
REFERENCE/DOCKET NUMBER: P-3126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 847 5317
TELEFAX: 201 848 9228
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-276-271-2

Query Match 100.0%; Score 29; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 agtcggtgtaggcaggttggtgact 29
|||||
2 agtcggtgtaggcaggttggtgact 30

RESULT 5
Sequence 6, Application US/08434465
Patent No. 6011020
GENERAL INFORMATION:
APPLICANT: LARRY GOLD, PAUL G. SCHMIDT, NEBOJSA JANJIC
TITLE OF INVENTION: NUCLEIC ACID LIGAND COMPLEXES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,465
FILING DATE: 4-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/234,997
FILING DATE: 28-APRIL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McClearn
REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 38
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:

OTHER INFORMATION: Nucleotides 37 and 38 are
bound by a phosphorothioate bond
US-08-434-465-6

Query Match 100.0%; Score 29; DB 3; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agtcggtgtaggcaggttggtgact 29
|||||
Db 2 agtcggtgtaggcaggttggtgact 30

RESULT 6
US-08-687-421-279
Sequence 279, Application US/08687421
Patent No. 6177557
GENERAL INFORMATION:
APPLICANT: Gold, Larry
APPLICANT: Janjic, Nebojsa
TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF BASIC
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR AND
TITLE OF INVENTION: THROMBIN
NUMBER OF SEQUENCES: 445
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,421
FILING DATE: 08-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/195,005
FILING DATE: 10-FEBRUARY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 22-APRIL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/219,012
FILING DATE: 28-MARCH-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,333
FILING DATE: 11-NOVEMBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX07/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 279:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-687-421-279

Query Match

Best Local Similarity 100.0%; Score 29; DB 4; Length 38;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 agtccgtgtagggcaggttgagggtgact 29
|||||
DB 2 agtccgtgtagggcaggttgagggtgact 30

RESULT 7

PCT-US95-09237-2

Sequence 2, Application PC/TUS9509237

GENERAL INFORMATION:

APPLICANT: Pitner, James B

APPLICANT: Malinowski, Douglas P

APPLICANT: Vonk, Glenn P

APPLICANT: Gold, Larry

TITLE OF INVENTION: Spectroscopically Detectable Nucleic

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson, Barry J.

STREET: 8400 E. Prentice Avenue, Suite 200

CITY: Englewood

STATE: CO

COUNTRY: USA

ZIP: 80111

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/09237

FILING DATE: 21 JULY 1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Swanson, Barry J.

REGISTRATION NUMBER: 33,215

REFERENCE/DOCKET NUMBER: NEX-BEC/PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 303 793 3333

TELEFAX: 303 793 3433

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

PCT-US95-09237-2

Query Match 100.0%; Score 29; DB 5; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 agtccgtgtagggcaggttgagggtgact 29
|||||
DB 2 agtccgtgtagggcaggttgagggtgact 30

RESULT 8

US-08-479-783A-90

Sequence 90, Application US/08479783A

Patent No. 5668264

GENERAL INFORMATION:

APPLICANT: NEBOJSA JANJIC

APPLICANT: LARRY GOLD

TITLE OF INVENTION: HIGH AFFINITY PDGF NUCLEIC

TITLE OF INVENTION: ACID LIGANDS

NUMBER OF SEQUENCES: 90

CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson and Bratschun, L.L.C.

STREET: 8400 East Prentice Avenue, Suite #200

CITY: Denver

STATE: Colorado

COUNTRY: USA

ZIP: 80111

COMPUTER READABLE FORM:

MEDIUM TYPE: diskette, 3.5 inch, 1.4 Mb storage

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/479,783A

FILING DATE: 7-JUNE-1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/714,131

FILING DATE: 10-JUNE-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/931,473

FILING DATE: 17-AUGUST-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/964,624

FILING DATE: 21-OCTOBER-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/117,991

FILING DATE: 8-SEPTEMBER-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/536,428

FILING DATE: 11-JUNE-1990

ATTORNEY/AGENT INFORMATION:

NAME: Diane H. McLearn

REGISTRATION NUMBER: 33,960

REFERENCE/DOCKET NUMBER: NEX42-2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3333

TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 90:

SEQUENCE CHARACTERISTICS:

LENGTH: 39 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

OTHER INFORMATION: Nucleotide 39 is an inverted

OTHER INFORMATION: orientation T (3'-3' linked)

US-08-479-783A-90

Query Match 100.0%; Score 29; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 agtccgtgtagggcaggttgagggtgact 29
|||||
DB 2 agtccgtgtagggcaggttgagggtgact 30

RESULT 9

US-08-479-725-90

Sequence 90, Application US/08479725

Patent No. 5674685

GENERAL INFORMATION:

APPLICANT: NEBOJSA JANJIC

APPLICANT: LARRY GOLD

TITLE OF INVENTION: HIGH AFFINITY PDGF NUCLEIC

NUMBER OF SEQUENCES: 90

CORRESPONDENCE ADDRESS:

ADDRESSER: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,725
FILING DATE: 7-JUNE-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McClearn
REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX42-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEO ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: Nucleotide 39 is an inverted
OTHER INFORMATION: orientation T (3'-3' linked)
US-08-479-725-90

Query Match: 100.0%; Score 29; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agtcctgtaggagcaggttgaggtgact 29
|||||
DB 2 AGTCCTGTTAGGAGCAGGTGAGGTGACT 30

RESULT 10
US-08-618-693-88
Sequence 88, Application US/08618693
Patent No. 5723594
GENERAL INFORMATION:
APPLICANT: NEBOJSA JANJIC
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY PDGF NUCLEIC
TITLE OF INVENTION: ACID LIGANDS
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESSES:
ADDRESSER: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver

STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,693
FILING DATE: 20 MARCH 1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,783
FILING DATE: 7-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX42/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEO ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: Nucleotide 39 is an
OTHER INFORMATION: inverted orientation T (3'-3' linked)
US-08-618-693-88

Query Match: 100.0%; Score 29; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agtcctgtaggagcaggttgaggtgact 29
|||||
DB 2 AGTCCTGTTAGGAGCAGGTGAGGTGACT 30

RESULT 11
US-08-973-124-177
Sequence 177, Application US/08973124
Patent No. 6207816
GENERAL INFORMATION:
APPLICANT: LARRY GOLD et al.
TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE
TITLE OF INVENTION: LIGANDS TO GROWTH
TITLE OF INVENTION: FACTORS
NUMBER OF SEQUENCES: 304
CORRESPONDENCE ADDRESSES:
ADDRESSER: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,124
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08014
FILING DATE: 30-MAY-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,423
FILING DATE: 02-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,424
FILING DATE: 02-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,594
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,591
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,725
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,783
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/618,693
FILING DATE: 20-MARCH-1996
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 177:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
OTHER INFORMATION: Nucleotide 39 is an
OTHER INFORMATION: Inverted orientation T (3'-3' linked)
US-08-973-124-177

Query Match 100.0%; Score 29; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 agtccgtgtaggcaggttgagggtgact 29
|||||
2 agtccgtgtaggcaggttgagggtgact 30

RESULT 12
US-08-991-743C-88
Sequence 88, Application US/08991743C
Patent No. 6229002
GENERAL INFORMATION:
APPLICANT: NEBOUSA JANJIC, LARRY GOLD
TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR (PDGF) NUCLEIC
ACID LIGAND COMPLEXES
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 1745 Shea Center Drive, Suite 330
CITY: Highlands Ranch
STATE: Colorado
COUNTRY: USA
ZIP: 80129
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,743C

FILING DATE: 16-Dec-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/618,693
FILING DATE: 20-MARCH-1996
APPLICATION NUMBER: 08/479,783
FILING DATE: 7-JUNE-1995
APPLICATION NUMBER: 08/479,725
FILING DATE: 7-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 268-0066
TELEFAX: (303) 268-0065
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: Nucleotide 39 is an inverted orientation T
(3'-3'-linked).
SEQUENCE DESCRIPTION: SEQ ID NO: 88:
US-08-991-743C-88

Query Match 100.0%; Score 29; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 agtccgtgtaggcaggttgagggtgact 29
|||||
2 agtccgtgtaggcaggttgagggtgact 30

Db 2 agtccgtgtaggcaggttgagggtgact 30

RESULT 13
PCT-US96-08014-177
Sequence 177, Application PC/TUS9608014
GENERAL INFORMATION:
APPLICANT: LARRY GOLD, NEBOUSA JANJIC, STEVEN RINGQUIST;
APPLICANT: PAGARITS, PENELOPE J. TOOTHMAN
TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE
TITLE OF INVENTION: LIGANDS TO TRANSFORMING GROWTH
TITLE OF INVENTION: FACTOR (TGF), PLATELET-DERIVED
TITLE OF INVENTION: GROWTH FACTOR (PDGF) AND HUMAN
TITLE OF INVENTION: KEROTINOCYTE GROWTH FACTOR (hKGF)
NUMBER OF SEQUENCES: 304
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08014
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,423
FILING DATE: 02-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,424
FILING DATE: 02-JUNE-1995
PRIOR APPLICATION DATA:

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? APPLICATION NUMBER: 08/465,594
? FILING DATE: 05-JUNE-1995
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/465,591
? FILING DATE: 05-JUNE-1995
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/479,725
? FILING DATE: 07-JUNE-1995
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/479,783
? FILING DATE: 07-JUNE-1995
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/618,693
? FILING DATE: 20-MARCH-1996
? ATTORNEY/AGENT INFORMATION:
? NAME: Barry J. Swanson
? REGISTRATION NUMBER: 33,215
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (303) 793-3333
? TELEFAX: (303) 793-3433
? INFORMATION FOR SEQ ID NO: 177:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 39 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA
? FEATURE:
? OTHER INFORMATION: Nucleotide 39 is an
? OTHER INFORMATION: Inverted orientation T (3'-3' linked)
PCT-US96-08014-177

Query Match 100.0%; Score 29; DB 5; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agtcctgtgtaagcaggttgagggtact 29
DB 2 AGTCCTGTGTAAGCAGGTGGGTGACT 30

RESULT 14
US-08-434-465-9
; Sequence 9, Application US/08434465
; Patent No. 6011020
; GENERAL INFORMATION:
; APPLICANT: LARRY GOLD, PAUL G. SCHMIDT, NEROJSA JANJIC
; TITLE OF INVENTION: NUCLEIC ACID LIGAND COMPLEXES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson and Bratschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,465
; FILING DATE: 4-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
```

```

? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/234,997
? FILING DATE: 28-April-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Diane H. McLearn
? REGISTRATION NUMBER: 33,960
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (303) 793-3333
? TELEFAX: (303) 793-3433
? INFORMATION FOR SEQ ID NO: 9:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 40
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA
? FEATURE:
? OTHER INFORMATION: N at position 1 is an alkyl
? OTHER INFORMATION: disulfide linker
? FEATURE:
? OTHER INFORMATION: N at position 38 is a dt amino
? OTHER INFORMATION: phosphoramidite
? OTHER INFORMATION: Inverted-orientation (3'-3' linkage) phosphoramidite
US-08-434-465-9

Query Match 100.0%; Score 29; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agtcctgtgtaagcaggttgagggtact 29
DB 3 AGTCCTGTGTAAGCAGGTGGGTGACT 31

RESULT 15
US-08-434-465-13
; Sequence 16, Application US/08434465
; Patent No. 6011020
; GENERAL INFORMATION:
; APPLICANT: LARRY GOLD, PAUL G. SCHMIDT, NEROJSA JANJIC
; TITLE OF INVENTION: NUCLEIC ACID LIGAND COMPLEXES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson and Bratschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,465
; FILING DATE: 4-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/234,997
; FILING DATE: 28-April-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Diane H. McLearn
```

Fri Jun 7 09:51:18 2002

us-09-599-220-2.rni

Page 8

1 REGISTRATION NUMBER: 33,960
 2 REFERENCE/DOCKET NUMBER: NEX9
 3 TELECOMMUNICATION INFORMATION:
 4 TELEPHONE: (303) 793-3333
 5 TELEFAX: (303) 793-3433
 6 INFORMATION FOR SEQ ID NO: 13:
 7 SEQUENCE CHARACTERISTICS:
 8 LENGTH: 40
 9 TYPE: nucleic acid
 10 STRANDEDNESS: single
 11 TOPOLOGY: linear
 12 MOLECULE TYPE: DNA
 13 FEATURE:
 14 OTHER INFORMATION: N at position 1 is a 20,000 MW
 15 OTHER INFORMATION: PEG
 16 FEATURE:
 17 OTHER INFORMATION: N at position 38 is a dT amino
 18 OTHER INFORMATION: phosphoramidite
 19 OTHER INFORMATION: Nucleotide 39 is an inverted
 20 OTHER INFORMATION: orientation (3'3' linkage) phosphoramidite

Query Match	100.0%	Score 29	DB 3	Length 40
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Search completed: June 6, 2002, 16:04:32
Job time: 1893 sec

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QY 1 ggttggtggttg 15
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Db 1 ggttggtggttg 15

RESULT 2

LOCUS AR009268 15 bp DNA linear PAT 04-DEC-1998

DEFINITION Sequence 31 from patent US 5756291.

ACCESSION AR009268

VERSION AR009268.1 GI:3968073

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 15)

AUTHORS Griffin,L., Albrecht,G., Latham,J., Leung,L., Vermaas,E. and Toole,J.J.

TITLE Aptamers specific for biomolecules and methods of making

JOURNAL Patent: US 5756291-A 31 26-MAY-1998;

FEATURES Location/Qualifiers

source 1..15

/organism="unknown"

BASE COUNT 0 a 0 c 9 g 6 t

ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggttggtggttg 15
|||||
Db 1 ggttggtggttg 15

RESULT 3

LOCUS AR009269 15 bp DNA linear PAT 04-DEC-1998

DEFINITION Sequence 32 from patent US 5756291.

ACCESSION AR009269

VERSION AR009269.1 GI:3968074

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 15)

AUTHORS Griffin,L., Albrecht,G., Latham,J., Leung,L., Vermaas,E. and Toole,J.J.

TITLE Aptamers specific for biomolecules and methods of making

JOURNAL Patent: US 5756291-A 32 26-MAY-1998;

FEATURES Location/Qualifiers

source 1..15

/organism="unknown"

BASE COUNT 0 a 0 c 9 g 6 t

ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 15;
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QY 1 ggttggtggttg 15
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Db 1 ggttggtggttg 15

RESULT 4

LOCUS AR009273 15 bp DNA linear PAT 04-DEC-1998

DEFINITION Sequence 36 from patent US 5756291.

ACCESSION AR009273

VERSION AR009273.1 GI:3968078

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 15)

AUTHORS Griffin,L., Albrecht,G., Latham,J., Leung,L., Vermaas,E. and Toole,J.J.

TITLE Aptamers specific for biomolecules and methods of making

JOURNAL Patent: US 5756291-A 36 26-MAY-1998;

FEATURES Location/Qualifiers

source 1..15

/organism="unknown"

BASE COUNT 0 a 0 c 9 g 6 t

ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggttggtggttg 15
|||||
Db 1 ggttggtggttg 15

RESULT 5

LOCUS AR009274 15 bp DNA linear PAT 04-DEC-1998

DEFINITION Sequence 37 from patent US 5756291.

ACCESSION AR009274

VERSION AR009274.1 GI:3968079

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 15)

AUTHORS Griffin,L., Albrecht,G., Latham,J., Leung,L., Vermaas,E. and Toole,J.J.

TITLE Aptamers specific for biomolecules and methods of making

JOURNAL Patent: US 5756291-A 37 26-MAY-1998;

FEATURES Location/Qualifiers

source 1..15

/organism="unknown"

BASE COUNT 0 a 0 c 9 g 6 t

ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggttggtggttg 15
|||||
Db 1 ggttggtggttg 15

RESULT 6

LOCUS AR009275 15 bp DNA linear PAT 04-DEC-1998

DEFINITION Sequence 38 from patent US 5756291.

ACCESSION AR009275

VERSION AR009275.1 GI:3968080

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 15)

AUTHORS Griffin,L., Albrecht,G., Latham,J., Leung,L., Vermaas,E. and Toole,J.J.

TITLE Aptamers specific for biomolecules and methods of making

JOURNAL Patent: US 5756291-A 38 26-MAY-1998;
FEATURES Location/Qualifiers
Source 1..15
/organism="unknown"
BASE COUNT 0 a 0 c 9 g 6 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3e+03;
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QY 1 ggttggtggtggtg 15
|||||
Db 1 GGTGGGTGCGTTGG 15

RESULT 7
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DEFINITION Sequence 79 from patent US 5756291.
ACCESSION AR009316
VERSION AR009316.1 GI:3968121
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Griffin,L., Albrecht,G., Latham,J., Leung,L., Vermaas,E. and
Tooie,J.J.
TITLE Aptamers specific for biomolecules and methods of making
JOURNAL Patent: US 5756291-A 79 26-MAY-1998;
FEATURES Location/Qualifiers
Source 1..15
/organism="unknown"

BASE COUNT 0 a 0 c 9 g 6 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggttggtggtggtg 15
|||||
Db 1 GGTGGGTGCGTTGG 15

RESULT 8
LOCUS AR060775 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 19 from patent US 5840867.
ACCESSION AR060775
VERSION AR060775.1 GI:5987225
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Tooie,J.J., Griffin,L.C., Bock,L.C. and Latham,J.A.
TITLE Aptamer analogs specific for biomolecules
JOURNAL Patent: US 5840867-A 19 24-NOV-1998;
FEATURES Location/Qualifiers
Source 1..15
/organism="unknown"

BASE COUNT 0 a 0 c 9 g 6 t
ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggttggtggtggtg 15
|||||
Db 1 GGTGGGTGCGTTGG 15

RESULT 9
LOCUS AR060777 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 21 from patent US 5840867.
ACCESSION AR060777
VERSION AR060777.1 GI:5987227
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Tooie,J.J., Griffin,L.C., Bock,L.C. and Latham,J.A.
TITLE Aptamer analogs specific for biomolecules
JOURNAL Patent: US 5840867-A 21 24-NOV-1998;
FEATURES Location/Qualifiers
Source 1..15
/organism="unknown"

BASE COUNT 0 a 0 c 9 g 6 t
ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 15;
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggttggtggtggtg 15
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Db 1 GGTGGGTGCGTTGG 15

RESULT 10
LOCUS AR060778 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 22 from patent US 5840867.
ACCESSION AR060778
VERSION AR060778.1 GI:5987228
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Tooie,J.J., Griffin,L.C., Bock,L.C. and Latham,J.A.
TITLE Aptamer analogs specific for biomolecules
JOURNAL Patent: US 5840867-A 22 24-NOV-1998;
FEATURES Location/Qualifiers
Source 1..15
/organism="unknown"

BASE COUNT 0 a 0 c 9 g 6 t
ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggttggtggtggtg 15
|||||
Db 1 GGTGGGTGCGTTGG 15

RESULT 11
LOCUS AR098723 15 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 81 from patent US 6077668.
ACCESSION AR098723
VERSION AR098723.1 GI:12808489
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 15)

AUTHORS Kool,E.T.

TITLE Highly sensitive multimeric nucleic acid probes

JOURNAL Patent: US 6077668-A 81 20-JUN-2000;

FEATURES

source 1..15
Location/Qualifiers

BASE COUNT 0 a 0 c 9 g 6 t

ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggttggtggtggtg 15

1 ggttggtggtggtg 15

RESULT 12

LOCUS ARI25847

DEFINITION Sequence 189 from patent US 6177557.

ACCESSION ARI25847

VERSION ARI25847.1 GI:14111909

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 15)

AUTHORS Janjic,N., Gold,L. and Tasset,D.

TITLE High affinity ligands of basic fibroblast growth factor and thrombin

JOURNAL Patent: US 6177557-A 189 23-JAN-2001;

FEATURES

source 1..15

BASE COUNT 0 a 0 c 9 g 6 t

ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggttggtggtggtg 15

1 ggttggtggtggtg 15

RESULT 13

LOCUS ARI68827

DEFINITION Sequence 53 from patent US 6288042.

ACCESSION ARI68827

VERSION ARI68827.1 GI:17904949

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 15)

AUTHORS Rando,R.F., Ojwang,J.O., Hogan,M.E., Wallace,T.L. and Cossum,P.A.

TITLE Anti-viral guanosine-rich tetrad forming oligonucleotides

JOURNAL Patent: US 6288042-A 53 11-SEP-2001;

FEATURES

source 1..15

BASE COUNT 0 a 0 c 9 g 6 t

ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggttggtggtggtg 15

1 ggttggtggtggtg 15

RESULT 14

LOCUS I16587

DEFINITION Sequence 1 from patent US 5476766.

ACCESSION I16587

VERSION I16587.1 GI:1251495

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 15)

AUTHORS Gold,L. and Tasset,D.

TITLE Ligands of thrombin

JOURNAL Patent: US 5476766-A 1 19-DEC-1995;

FEATURES

source 1..15

BASE COUNT 0 a 0 c 9 g 6 t

ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggttggtggtggtg 15

1 ggttggtggtggtg 15

RESULT 15

LOCUS I24214

DEFINITION Sequence 1 from patent US 5543293.

ACCESSION I24214

VERSION I24214.1 GI:1604084

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 15)

AUTHORS Gold,L. and Tasset,D.

TITLE DNA ligands of thrombin

JOURNAL Patent: US 5543293-A 1 06-AUG-1996;

FEATURES

source 1..15

BASE COUNT 0 a 0 c 9 g 6 t

ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 ggttggtggtggtg 15

Search completed: June 6, 2002, 16:03:19
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 6, 2002, 15:32:59 ; Search time 234.25 Seconds
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Title:	US-09-599-220-1
Perfect score:	15
Sequence:	1 ggttggtgtgttg 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 1905168
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minimum DB seq length: 0
maximum DB seq length: 50

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Post-processing: Minimum Match 0%
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SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	15	100.0	15	13	AAQ28472	Thrombin aptamer.
2	15	100.0	15	13	AAQ28474	Modified Thrombin
3	15	100.0	15	13	AAQ28477	Modified Thrombin
4	15	100.0	15	13	AAQ28478	Modified Thrombin
5	15	100.0	15	13	AAQ28475	Modified Thrombin
6	15	100.0	15	13	AAQ28476	Modified Thrombin
7	15	100.0	15	13	AAQ28479	Modified Thrombin
8	15	100.0	15	13	AAQ28480	Modified Thrombin
9	15	100.0	15	13	AAQ28481	Modified Thrombin

10	15	100.0	15	15	AA063005	g15d ligand to thr
11	15	100.0	15	17	AA866653	Spectroscopically
12	15	100.0	15	17	AAT28615	Quadruplex/duplex
13	15	100.0	15	17	AAT17808	Glycosaminoglycan
14	15	100.0	15	18	AAT51669	Viral integrase in
15	15	100.0	15	18	AA85811	Thrombin-binding n
16	15	100.0	15	18	AA88048	Thrombin-binding 1
17	15	100.0	15	19	AA879251	Oligonucleotide #4
18	15	100.0	15	19	AAV60407	Thrombin-binding a
19	15	100.0	15	19	AAV60408	Thrombin-binding a
20	15	100.0	15	19	AAV60409	Thrombin-binding a
21	15	100.0	15	19	AAV60400	Modified thrombin-a
22	15	100.0	15	19	AAV60402	Thioate linked thr
23	15	100.0	15	19	AAV60403	Thioate linked thr
24	15	100.0	15	19	AAV60450	Consensus sequence
25	15	100.0	15	19	AA97947	G-quartet oligonuc
26	15	100.0	15	19	AA833613	Thrombin inhibitor
27	15	100.0	15	20	AA830059	DNA oligonucleoid
28	15	100.0	15	20	AA825874	Nucleic acid ligand
29	15	100.0	15	20	AA825877	Reversing agent #2
30	15	100.0	15	22	AA870727	Oligonucleotide G1
31	15	100.0	15	22	AA824185	Tight binding comp
32	15	100.0	15	22	AA891744	Thrombin-binding a
33	15	100.0	15	22	AA88063	Thrombin aptamer b
34	15	100.0	17	13	AA028473	Modified thrombin
35	15	100.0	17	18	AA825670	Viral integrase in
36	15	100.0	17	19	AA879252	Oligonucleotide #4
37	15	100.0	17	19	AAV60401	MEK-linked thrombi
38	15	100.0	17	19	AAV60484	Thrombin-binding a
39	15	100.0	17	19	AAV60470	Thrombin-binding a
40	15	100.0	18	18	AAT51671	Viral integrase in
41	15	100.0	18	19	AA879253	Oligonucleotide #4
42	15	100.0	19	22	AA88064	Thrombin aptamer b
43	15	100.0	20	22	AA888065	Thrombin aptamer b
44	15	100.0	20	22	AA888066	Thrombin aptamer b
45	15	100.0	21	22	AA888066	Thrombin aptamer b

ALIGNMENTS

RESULT	1
AAQ28472	
ID	AAQ28472 standard; DNA; 15 bp.
XX	
AC	AAQ28472;
XX	
DT	16-FEB-1993 (first entry)
XX	
DE	Thrombin aptamer.
XX	
KW	Aptamer; specifically binding oligonucleotides; primer/linker; PCR
KW	cleavage; ss.
XX	
OS	Synthetic.
XX	
PN	WO9214843-A.
XX	
PD	03-SEP-1992.
XX	
PF	21-FEB-1992; 92WO-US01383.
XX	
PR	21-FEB-1991; 91US-0658796.
PR	21-FEB-1991; 91US-0658849.
PR	21-FEB-1991; 91US-0659103.
PR	21-FEB-1991; 91US-0659113.
PR	21-FEB-1991; 91US-0659114.
PR	21-FEB-1991; 91US-0659980.
PR	21-FEB-1991; 91US-0659981.
PR	14-AUG-1991; 91US-0744870.
PR	14-AUG-1991; 91US-0745215.
PR	06-NOV-1991; 91US-0787921.
XX	

PA	(GILE-) GILEAD SCI INC.
PX	
PI	Bock LC, Griffin LC, Krawczyk S, Latham JA, Tooile JT;
PL	Muenchau DD;
PX	
DR	WPI; 1992-316194/38.
PX	
PT	DNA aptamers specifically binding target molecules - useful for
PR	retrieving target molecules, delivering drugs or toxins to
PP	desired targets and for treating auto-immune diseases
PX	
PS	Disclosure; Page 119; 183pp; English.
PX	
CC	The sequences given in AAQ28473-78 are aptamers which are based on the
CC	unmodified thrombin aptamer given in AAQ28472. These aptamers bind
CC	to thrombin inhibiting its activity, except for the aptamer sequence
CC	given in AAQ28475 which was required in very large quantities to inhibit
CC	thrombin activity. These aptamers are stable, versatile and highly
CC	specific to their intended targets. They can be used to deliver
CC	auxiliary substances, eg. drugs, toxins, radio isotopes etc. to a
CC	specific part of the body. The aptamers have a binding region of
SQ	approx. 10 nucleotide residues.
PX	
SQ	Sequence 15 BP; 0 A; 0 C; 9 G; 6 T; 0 other;
OY	
Db	Query Match 100.0%; Score 15; DB 13; Length 15; Best Local Similarity 100.0%; Pred. No. 4.4e+02; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 ggttggtggtgg 15 1 ggttggtggtgg 15
RESULT 2	
ID	AAQ28474
XX	AAQ28474 standard; DNA; 15 BP.
AC	
XX	AAQ28474:
DT	16-FEB-1993 (first entry)
XX	
DE	Modified thrombin aptamer #2.
XX	
KM	Aptamer; specifically binding oligonucleotides; primer/linker; PCR;
KM	Cleavage; ss.
XX	
XX	Synthetic.
FT	Key Location/Qualifiers
FT	misc_difference 13..14
FT	/tag= a
FT	/note= "The linkage between T13 and G14 is a
FT	thioate linkage"
FT	misc_difference 14..15
FT	/tag= b
FT	/note= "The linkage between G14 and G15 is a
FT	thioate linkage"
PN	WO9214843-A.
PD	03-SEP-1992.
PX	
XX	21-FEB-1992; 92WO-US01383.
PX	
PR	21-FEB-1991; 91US-0658796.
PR	21-FEB-1991; 91US-0658849.
PR	21-FEB-1991; 91US-0659103.
PR	21-FEB-1991; 91US-0659113.
PR	21-FEB-1991; 91US-0659114.
PR	21-FEB-1991; 91US-0659980.
PR	21-FEB-1991; 91US-0659981.

PR	14-AUG-1991:	91US-0744870.
PR	14-AUG-1991:	91US-0745215.
PR	06-NOV-1991:	91US-0787921.
XX		
PA	(GILE-) GILEAD SCI INC.	
XX		
PI	Bock LC, Griffin LE, Krawczyk S, Latham JA, Toole JJ;	
PI	Menichau DD;	
XX		
DR	WPI, 1992-316194/38.	
XX		
PT	DNA aptamers specifically binding target molecules - useful for	
PT	retrieving target molecules, delivering drugs or toxins to	
PT	desired targets and for treating auto-immune diseases	
XX		
PS	Disclosure; Page 119; 183pp; English.	
XX		
CC	The sequences given in AAQ28473-78 are aptamers which are based on the	
CC	unmodified thrombin aptamer given in AAQ28472. These aptamers bind	
CC	to thrombin inhibiting its activity, except for the aptamer sequence	
CC	given in AAQ28475 which was required in very large quantities to inhibit	
CC	thrombin activity. These aptamers are stable, versatile and highly	
CC	specific to their intended targets. They can be used to deliver	
CC	auxiliary substances, eg. drugs, toxins, radio isotopes etc. to a	
CC	specific part of the body. The aptamers have a binding region of	
CC	approx. 10 nucleotide residues.	
XX		
SQ	Sequence 15 BP; 0 A; 0 C; 9 G; 6 T; 0 other;	
	Query Match 100.0%; Score 15; DB 13; Length 15;	
	Best Local Similarity 100.0%; Pred. No. 4,4e+02;	
	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 gtttggtggtggtcg 15	
DB	1 gttggtggtggtcg 15	
RESULT 3		
AAQ28477		
ID	AAQ28477 standard; DNA; 15 BP.	
XX		
AC	AAQ28477;	
XX		
DT	16-FEB-1993 (first entry)	
XX		
DE	Modified thrombin aptamer #5.	
XX		
KW	Aptamer; specifically binding oligonucleotides; primer/linker; PCR;	
KW	cleavage; ss.	
XX		
OS	Synthetic.	
XX		
FT	Key Location/Qualifiers	
FT	modified_base 3	
FT	/*tag= a	
FT	/label= 5-(1-pentynyl)-2'-deoxyuridine	
FT	modified_base 12	
FT	/*tag= b	
FT	/label= 5-(1-pentynyl)-2'-deoxyuridine	
XX		
PN	W09214843-A.	
XX		
XX		
PD	03-SEP-1992.	
XX		
PF	21-FEB-1992; 92WO-US01383.	
XX		
PR	21-FEB-1991; 91US-0658796.	
PR	21-FEB-1991; 91US-0658849.	
PR	21-FEB-1991; 91US-0659103.	
PR	21-FEB-1991; 91US-0659113.	
PR	21-FEB-1991; 91US-0659114.	


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PR 21-FEB-1991; 91US-0659980.
PR 21-FEB-1991; 91US-0659981.
PR 14-AUG-1991; 91US-0744870.
PR 14-AUG-1991; 91US-0745215.
PR 06-NOV-1991; 91US-0787921.
XX
PA (GILE-) GILEAD SCI INC.
XX
PI Bock LC, Griffin LC, Krawczyk S, Latham JA, Tooie JJ;
PI Muenchau DD;
XX
DR WPI; 1992-316194/38.
XX
PT DNA aptamers specifically binding target molecules - useful for
PT retrieving target molecules, delivering drugs or toxins to
PT desired targets and for treating auto-immune diseases
XX
PS Disclosure; Page 119; 183pp; English.
XX
CC The sequences given in AAQ28473-78 are aptamers which are based on the
CC unmodified thrombin aptamer given in AAQ28472. These aptamers bind
CC to thrombin inhibiting its activity, except for the aptamer sequence
CC given in AAQ28475 which was required in very large quantities to inhibit
CC thrombin activity. These aptamers are stable, versatile and highly
CC specific to their intended targets. They can be used to deliver
CC auxiliary substances, eg. drugs, toxins, radio isotopes etc. to a
CC specific part of the body. The aptamers have a binding region of
CC approx. 10 nucleotide residues.
XX
SQ Sequence 15 BP; 0 A; 0 C; 9 G; 4 T; 0 other;

Query Match 100.0%; Score 15; DB 13; Length 15;
Best Local Similarity 86.7%; Pred. No. 4.4e+02;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggttggtgtgtgtg 15
   ||:|||||:||||
Db 1 ggttggtgtgtg 15

RESULT 4
AAQ28478
ID AAQ28478 standard; DNA; 15 BP.
XX
AC AAQ28478;
XX
DT 16-FEB-1993 (first entry)
XX
DE Modified thrombin aptamer #6.
XX
KW Aptamer; specifically binding oligonucleotides; primer/linker; PCR;
KW cleavage; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT 13
FT modified_base /tag= a
FT /label= 5-(1-pentynyl)uracil
XX
PN WO9214843-A.
XX
PD 03-SEP-1992.
XX
PF 21-FEB-1992; 92WO-US01383.
XX
PR 21-FEB-1991; 91US-0658796.
PR 21-FEB-1991; 91US-0658849.
PR 21-FEB-1991; 91US-0659103.
PR 21-FEB-1991; 91US-0659113.
PR 21-FEB-1991; 91US-0659114.
PR 21-FEB-1991; 91US-0659980.
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PR 21-FEB-1991; 91US-0659981.
PR 14-AUG-1991; 91US-0744870.
PR 14-AUG-1991; 91US-0745215.
PR 06-NOV-1991; 91US-0787921.
XX
PA (GILE-) GILEAD SCI INC.
XX
PI Bock LC, Griffin LC, Krawczyk S, Latham JA, Tooie JJ;
PI Muenchau DD;
XX
DR WPI; 1992-316194/38.
XX
PT DNA aptamers specifically binding target molecules - useful for
PT retrieving target molecules, delivering drugs or toxins to
PT desired targets and for treating auto-immune diseases
XX
PS Disclosure; Page 119; 183pp; English.
XX
CC The sequences given in AAQ28473-78 are aptamers which are based on the
CC unmodified thrombin aptamer given in AAQ28472. These aptamers bind
CC to thrombin inhibiting its activity, except for the aptamer sequence
CC given in AAQ28475 which was required in very large quantities to inhibit
CC thrombin activity. These aptamers are stable, versatile and highly
CC specific to their intended targets. They can be used to deliver
CC auxiliary substances, eg. drugs, toxins, radio isotopes etc. to a
CC specific part of the body. The aptamers have a binding region of
CC approx. 10 nucleotide residues.
XX
SQ Sequence 15 BP; 0 A; 0 C; 9 G; 5 T; 0 other;

Query Match 100.0%; Score 15; DB 13; Length 15;
Best Local Similarity 93.3%; Pred. No. 4.4e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggttggtgtgtgtg 15
   |||||||:||||:|
Db 1 ggttggtgtgtg 15

RESULT 5
AAQ28475
ID AAQ28475 standard; DNA; 15 BP.
XX
AC AAQ28475;
XX
DT 16-FEB-1993 (first entry)
XX
DE Modified thrombin aptamer #3.
XX
KW Aptamer; specifically binding oligonucleotides; primer/linker; PCR;
KW cleavage; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT 1..2 /tag= a
FT misc_difference 1..2 /note= "The linkage between G1 and G2 is a
FT thioate linkage"
FT 2..3 /tag= b
FT misc_difference 2..3 /note= "The linkage between G2 and T3 is a
FT thioate linkage"
FT 3..4 /tag= c
FT misc_difference 3..4 /note= "The linkage between T3 and T4 is a
FT thioate linkage"
FT 4..5 /tag= d
FT misc_difference 4..5 /note= "The linkage between T4 and G5 is a
FT thioate linkage"
FT 5..6 misc_difference 5..6
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FT      /*tag-
FT      /note=
FT      "The linkage between G5 and G6 is a
FT      thioate linkage"
FT      misc_difference 6..7
FT      /*tag=
FT      /note=
FT      "The linkage between G6 and T7 is a
FT      thioate linkage"
FT      misc_difference 7..8
FT      /*tag=
FT      /note=
FT      "The linkage between T7 and G8 is a
FT      thioate linkage"
FT      misc_difference 8..9
FT      /*tag=
FT      /note=
FT      "The linkage between G8 and T9 is a
FT      thioate linkage"
FT      misc_difference 9..10
FT      /*tag=
FT      /note=
FT      "The linkage between T9 and G10 is a
FT      thioate linkage"
FT      misc_difference 10..11
FT      /*tag=
FT      /note=
FT      "The linkage between G10 and G11 is a
FT      thioate linkage"
FT      misc_difference 11..12
FT      /*tag=
FT      /note=
FT      "The linkage between G11 and T12 is a
FT      thioate linkage"
FT      misc_difference 12..13
FT      /*tag=
FT      /note=
FT      "The linkage between T12 and T13 is a
FT      thioate linkage"
FT      misc_difference 13..14
FT      /*tag=
FT      /note=
FT      "The linkage between T13 and G14 is a
FT      thioate linkage"
FT      misc_difference 14..15
FT      /*tag=
FT      /note=
FT      "The linkage between G14 and G15 is a
FT      thioate linkage"
FT      W09214843-A.
FT      03-SEP-1992.
FT      21-FEB-1992; 92WO-US01383.
FT      21-FEB-1991; 91US-0658796.
FT      21-FEB-1991; 91US-0658849.
FT      21-FEB-1991; 91US-0659103.
FT      21-FEB-1991; 91US-0659113.
FT      21-FEB-1991; 91US-0659114.
FT      21-FEB-1991; 91US-0659980.
FT      21-FEB-1991; 91US-0659981.
FT      21-FEB-1991; 91US-0744870.
FT      14-AUG-1991; 91US-0744870.
FT      14-AUG-1991; 91US-0745215.
FT      06-NOV-1991; 91US-0787921.
FT      (GILE-) GILEAD SCI INC.
FT      Bock LC, Griffin LC, Krawczyk S, Latham JA, Toole JI;
FT      Muenchau DD;
FT      WPI; 1992-316194/38.
FT      DNA aptamers specifically binding target molecules - useful for
FT      retrieving target molecules, delivering drugs or toxins to
FT      desired targets and for treating auto-immune diseases
FT      Disclosure; Page 119; 183pp; English.
FT      The sequences given in AAQ28473-78 are aptamers which are based on the
FT      unmodified thrombin aptamer given in AAQ28472. These aptamers bind
FT      to thrombin inhibiting its activity, except for the aptamer sequence

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CC      given in AAQ28475 which was required in very large quantities to inhibit
CC      thrombin activity. These aptamers are stable, versatile and highly
CC      specific to their intended targets. They can be used to deliver
CC      auxiliary substances, eg. drugs, toxins, radio isotopes etc. to a
CC      specific part of the body. The aptamers have a binding region of
CC      approx. 10 nucleotide residues.
CC      Sequence 15 BP; 0 A; 0 C; 9 G; 6 T; 0 other;
SQ
Query Match      100.0%; Score 15; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 4,4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 ggttggtggttg 15
DB      1 ggttggtggttg 15
RESULT 6
AAQ28476
ID      AAQ28476 standard; DNA; 15 BP.
AC      AAQ28476;
DT      16-FEB-1993 (first entry)
DE      Modified thrombin aptamer #4.
XX      Aptamer; specifically binding oligonucleotides; primer/linker; PCR;
XX      cleavage; ss.
XX      Synthetic.
XX      OS
XX      Key      Location/Qualifiers
FT      modified_base 7 /*tag= a
FT      modified_base 9 /label= 5-(1-pentynyl)-2'-deoxyuridine
FT      modified_base 9 /*tag= b
FT      /label= 5-(1-pentynyl)-2'-deoxyuridine
XX      W09214843-A.
XX      03-SEP-1992.
XX      21-FEB-1992; 92WO-US01383.
XX      21-FEB-1991; 91US-0658796.
XX      21-FEB-1991; 91US-0658849.
XX      21-FEB-1991; 91US-0659103.
XX      21-FEB-1991; 91US-0659113.
XX      21-FEB-1991; 91US-0659114.
XX      21-FEB-1991; 91US-0659980.
XX      21-FEB-1991; 91US-0659981.
XX      21-FEB-1991; 91US-0744870.
XX      14-AUG-1991; 91US-0745215.
XX      06-NOV-1991; 91US-0787921.
XX      (GILE-) GILEAD SCI INC.
XX      Bock LC, Griffin LC, Krawczyk S, Latham JA, Toole JI;
XX      Muenchau DD;
XX      WPI; 1992-316194/38.
XX      DNA aptamers specifically binding target molecules - useful for
XX      retrieving target molecules, delivering drugs or toxins to
XX      desired targets and for treating auto-immune diseases
XX      Disclosure; Page 119; 183pp; English.
XX      The sequences given in AAQ28473-78 are aptamers which are based on the
CC

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```
CC unmodified thrombin aptamer given in AAQ28472. These aptamers bind
CC to thrombin inhibiting its activity, except for the aptamer sequence
CC given in AAQ28475 which was required in very large quantities to inhibit
CC thrombin activity. These aptamers are stable, versatile and highly
CC specific to their intended targets. They can be used to deliver
CC auxiliary substances, eg. drugs, toxins, radio isotopes etc. to a
CC specific part of the body. The aptamers have a binding region of
CC approx. 10 nucleotide residues.
XX
SQ Sequence 15 BP; 0 A; 0 C; 9 G; 4 T; 0 other;

Query Match          100.0%; Score 15; DB 13; Length 15;
Best Local Similarity 86.7%; Pred. No. 4.4e+02;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ggttggtgtgttg 15
    |||||:|||||
Db 1 gtttguguggttg 15

RESULT 7
ID AAQ28479 standard; DNA; 15 BP.
XX
AC AAQ28479;
XX
DT 16-FEB-1993 (first entry)
XX
DE Modified thrombin aptamer #7.
XX
KM Aptamer; specifically binding oligonucleotides; primer/linker; PCR;
KW cleavage; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc-difference 3..4 /tag= a
FT /note= "The linkage between T3 and T4 is a
FT formacetal internucleotide linkage"
FT
XX
PN WO9214843-A.
XX
PD 03-SEP-1992.
XX
PR 21-FEB-1992; 92WO-US01383.
XX
PR 21-FEB-1991; 91US-0658796.
XX
PR 21-FEB-1991; 91US-0658849.
XX
PR 21-FEB-1991; 91US-0659103.
XX
PR 21-FEB-1991; 91US-0659113.
XX
PR 21-FEB-1991; 91US-0659114.
XX
PR 21-FEB-1991; 91US-0659980.
XX
PR 21-FEB-1991; 91US-0659981.
XX
PR 14-AUG-1991; 91US-0744870.
XX
PR 14-AUG-1991; 91US-0745215.
XX
PR 06-NOV-1991; 91US-0787921.
XX
XX
PA (GILE-) GILEAD SCI INC.
XX
PI Bock LC, Griffin LC, Krawczyk S, Latham JA, Toole JJ;
PI Muenchau DD;
XX
DR WPI; 1992-316194/38.
XX
PT DNA aptamers specifically binding target molecules - useful for
PT retrieving target molecules, delivering drugs or toxins to
PT desired targets and for treating auto-immune diseases
XX
PS Disclosure; Page 121; 183pp; English.
XX
CC The sequences given in AAQ28479-81 are aptamers which are based on the
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CC unmodified thrombin aptamer given in AAQ28472. These aptamers all
CC contain at least one formacetal internucleotide linkages. These
CC aptamers bind to thrombin inhibiting its activity. These aptamers
CC are stable, versatile and highly specific to their intended targets.
CC They can be used to deliver auxiliary substances, eg. drugs, toxins,
CC radio isotopes etc. to a specific part of the body. The aptamers have
CC a binding region of approx. 10 nucleotide residues.
XX
SQ Sequence 15 BP; 0 A; 0 C; 9 G; 6 T; 0 other;

Query Match          100.0%; Score 15; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ggttggtgtgttg 15
    |||||:|||||
Db 1 gtttggtgtgttg 15

RESULT 8
ID AAQ28480 standard; DNA; 15 BP.
XX
AC AAQ28480;
XX
DT 16-FEB-1993 (first entry)
XX
DE Modified thrombin aptamer #8.
XX
KM Aptamer; specifically binding oligonucleotides; primer/linker; PCR;
KW cleavage; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc-difference 12..13 /tag= a
FT /note= "The linkage between T12 and T13 is a
FT formacetal internucleotide linkage"
FT
XX
PN WO9214843-A.
XX
PD 03-SEP-1992.
XX
PR 21-FEB-1992; 92WO-US01383.
XX
PR 21-FEB-1991; 91US-0658796.
XX
PR 21-FEB-1991; 91US-0658849.
XX
PR 21-FEB-1991; 91US-0659103.
XX
PR 21-FEB-1991; 91US-0659113.
XX
PR 21-FEB-1991; 91US-0659114.
XX
PR 21-FEB-1991; 91US-0659980.
XX
PR 21-FEB-1991; 91US-0659981.
XX
PR 14-AUG-1991; 91US-0744870.
XX
PR 14-AUG-1991; 91US-0745215.
XX
PR 06-NOV-1991; 91US-0787921.
XX
XX
PA (GILE-) GILEAD SCI INC.
XX
PI Bock LC, Griffin LC, Krawczyk S, Latham JA, Toole JJ;
PI Muenchau DD;
XX
DR WPI; 1992-316194/38.
XX
PT DNA aptamers specifically binding target molecules - useful for
PT retrieving target molecules, delivering drugs or toxins to
PT desired targets and for treating auto-immune diseases
XX
PS Disclosure; Page 121; 183pp; English.
XX
CC The sequences given in AAQ28479-81 are aptamers which are based on the
CC unmodified thrombin aptamer given in AAQ28472. These aptamers all
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CC contain at least one formacetal internucleotide linkages. These
 CC aptamers bind to thrombin inhibiting its activity. These aptamers
 CC are stable, versatile and highly specific to their intended targets.
 CC They can be used to deliver auxiliary substances, eg. drugs, toxins,
 CC radio isotopes etc. to a specific part of the body. The aptamers have
 CC a binding region of approx. 10 nucleotide residues.
 CC
 SO Sequence 15 BP; 0 A; 0 C; 9 G; 6 T; 0 other;

Query Match 100.0%; Score 15; DB 13; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggttggtggtggtg 15
 |||
 Db 1 ggttggtggtggtg 15

RESULT 9
 ID AAQ28481 standard; DNA: 15 BP.
 AC AAQ28481;

DF 16-FEB-1993 (first entry)

DE Modified thrombin aptamer #9.

KM Aptamer; specifically binding oligonucleotides; primer/linker; PCR;
 cleavage; ss.

OS Synthetic.

Key Location/Qualifiers
 misc_difference 12..13

FT /*tag- a
 FT /note- "The linkage between T12 and T13 is a
 formacetal internucleotide linkage"

PN WO9214843-A.

PD 03-SEP-1992.

PF 21-FEB-1992; 92WO-US01383.

PR 21-FEB-1991; 91US-0658796.

PR 21-FEB-1991; 91US-0658849.

PR 21-FEB-1991; 91US-0659103.

PR 21-FEB-1991; 91US-0659113.

PR 21-FEB-1991; 91US-0659114.

PR 21-FEB-1991; 91US-0659860.

PR 21-FEB-1991; 91US-0659861.

PR 14-AUG-1991; 91US-0744870.

PR 14-AUG-1991; 91US-0745215.

PR 06-NOV-1991; 91US-0787921.

PA (GILE-) GILEAD SCI INC.

PI Bock LC, Griffin LC, Krawczyk S, Latham JA, Tooole JJ;
 PI Muenchau DD;

WPI; 1992-316194/38.

PT DNA aptamers specifically binding target molecules - useful for
 PT retrieving target molecules, delivering drugs or toxins to
 PT desired targets and for treating auto-immune diseases

PS Disclosure; Page 121; 183pp; English.

CC The sequences given in AAQ28479-81 are aptamers which are based on the
 CC unmodified thrombin aptamer given in AAQ28472. These aptamers all
 CC contain at least one formacetal internucleotide linkages. These

CC aptamers bind to thrombin inhibiting its activity. These aptamers
 CC are stable, versatile and highly specific to their intended targets.
 CC They can be used to deliver auxiliary substances, eg. drugs, toxins,
 CC radio isotopes etc. to a specific part of the body. The aptamers have
 CC a binding region of approx. 10 nucleotide residues.
 CC
 SO Sequence 15 BP; 0 A; 0 C; 9 G; 6 T; 0 other;

Query Match 100.0%; Score 15; DB 13; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggttggtggtggtg 15
 |||
 Db 1 ggttggtggtggtg 15

RESULT 10
 ID AAQ63005 standard; DNA: 15 BP.
 AC AAQ63005;

DF 07-NOV-1994 (first entry)

DE G1SD ligand to thrombin.

KM Thrombin; coagulation; adhesion; blood clot; clot formation;
 ligand; binding; ss.

OS Synthetic.

PN WO9408050-A.

PD 14-APR-1994.

PF 28-SEP-1993; 93WO-US09296.

PR 29-SEP-1992; 92US-0953694.

PR 21-OCT-1992; 92US-0964624.

PR 06-NOV-1992; 92US-0973333.

PR 22-APR-1993; 93US-0061691.

PA (NEXA-) NEXAGEN INC.

PI Gold LM, Janjic N, Tasset D, Tuerk C;

WPI; 1994-135610/16.

PT Producing target specific nucleic acid ligands - by selection for
 PT high affinity then structure determination, esp directed against
 PT HIV proteins, thrombin or basic fibroblast growth factor

PS Disclosure; Page 20; 208pp; English.

CC The synthetic ligand was produced by a method identical to the SELEX
 CC procedure. The ligand can prevent clot formation in vitro.

SO Sequence 15 BP; 0 A; 0 C; 9 G; 6 T; 0 other;

Query Match 100.0%; Score 15; DB 15; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggttggtggtggtg 15
 |||
 Db 1 ggttggtggtggtg 15

RESULT 11
 AA186653

XX	AAR86653 standard; DNA; 15 BP.
AC	AAT86653;
DT	08-MAY-1998 (first entry)
DE	Spectroscopically detectable nucleic acid ligand compound #1.
KW	Spectroscopically detectable; detection; phosphorothioate; fluorescein; thiazole orange; ss.
OS	Synthetic.
FH	Key
FT	modified_base 1 Location/Qualifiers
FT	/tag= a
FT	/note= "Guanine1 optionally labeled with fluorescein via a C6 linker molecule or labeled with Thiazole orange via a C3 linker"
FT	misc_feature 6..7 /tag= b
FT	/note= "Guanine6 and Thymine7 optionally linked via a phosphorothioate bond"
FT	modified_base 7 /tag= c
FT	/note= "Thymine7 phosphorothioate when present is linked to fluorescein via iodoacetamide."
PN	WO9622383-A1.
XX	25-JUL-1996.
PE	21-JUL-1995; 95WO-US09237.
PR	20-JAN-1995; 95US-0376329.
PA	(BECT) BECTON DICKINSON CO. (NEXS-) NEXSTAR PHARM INC.
PI	Goid L, Malinowski DP, Pitner JB, Vonk GP;
DR	WPI: 1996-354540/35.
PT	Detection of target cpds, such as thrombin - using spectroscopically detectable nucleic acid ligands
PS	Claims 7 and 11; Figure 1; 37pp; English.
CC	This sequence represents spectroscopically detectable nucleic acid ligands which were used to detect the presence or absence of a target compound (thrombin) in a sample. This ligand can also be used for monitoring the binding of target compounds (such as growth factors) to their receptors in competition-based assays. It is thus useful in diagnostic assays. Spectroscopically detectable nucleic acid ligands of the invention may be used to detect e.g. thrombin, elastase, cell surface markers, growth factors, growth factor receptors, whole cells or viral particles present in biological samples such as blood. The receptor molecules are typically relatively small in relation to traditional receptor molecules such as antibodies. Any additional weight or volume added to the receptor molecules (even in the form of a small target) will significantly increase the weight or volume of the labelled receptor molecule and therefore permit detection of the relatively significant energy differences involved (between bound and unbound labelled receptor molecules).
SO	Sequence 15 BP; 0 A; 0 C; 9 G; 6 T; 0 other:
OY	Query Match 100.0%; Score 15; DB 17; Length 15; Best Local Similarity 100.0%; Pred. No. 4,4e+02; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB	1	ggttggtggtggtg 15
RESULT	12	
ID	AA128615	
AC	AA128615	standard; DNA; 15 BP.
XX	AA128615;	
XX	14-NOV-1996	(first entry)
DE	Quadruplex/duplex thrombin inhibitor consensus sequence #3.	
XX	Thrombin; inhibitor; quadruplex/duplex structure; multimeric compound;	
KW	quadruplex motif; telomerase; nuclease resistant; diagnostic probe;	
KW	therapy; ss.	
XX	Synthetic.	
OS		
XX	Key	Location/Qualifiers
FH	misc_feature	1..2
FT	misc_feature	/tag= a
FT	misc_feature	/note= "bases involved in quadruplex formation"
FT	misc_feature	4
FT	misc_feature	/tag= b
FT	misc_feature	/note= "forms base pair with T at position 13"
FT	misc_feature	5..6
FT	misc_feature	/tag= c
FT	misc_feature	/note= "bases involved in quadruplex formation"
FT	misc_feature	10..11
FT	misc_feature	/tag= d
FT	misc_feature	/note= "bases involved in quadruplex formation"
FT	misc_feature	13
FT	misc_feature	/tag= e
FT	misc_feature	/note= "forms base pair with T at position 4"
FT	misc_feature	14..15
FT	misc_feature	/tag= f
FT	misc_feature	/note= "bases involved in quadruplex formation"
XX	WO9611010-A1.	
XX	18-APR-1996.	
XX	20-SEP-1995;	95WO-US11985.
XX	07-OCT-1994;	94US-0320139.
XX	(PHAR-) PHARMAGENICS INC.	
XX	Bertelsen AH, Beutel BA, Cook AF, Gao H, Joesten ME;	
PI	Macaya RF;	
XX	WPI; 1996-209651/21.	
DR		
XX	Single stranded oligo:deoxy:ribonucleotide thrombin inhibitors -	
XX	comprise quadruplex consensus motif either flanked by complementary	
PT	sequences which form duplex-stem or having bridged termini	
XX		
XX	Example; Page 41; 61pp: English.	
XX		
CC	AA128613-T28615, and AA128626 represent consensus sequences for the	
CC	thrombin inhibitors of the invention. The sequences can be used to	
CC	inhibit and to detect thrombin activity. These sequences form	
CC	quadruplex/duplex structures, and can also form multimeric compounds.	
CC	The inhibitors of the invention bind thrombin with a higher affinity than	
CC	quadruplex structures that lack the duplex stem (such as this sequence).	
CC	By bridging the 5' and 3' ends of these structures may optimise their use	
CC	as inhibitors to targets other than thrombin, such as telomerase. The	
CC	secondary structures formed by these sequences result in molecules which	
CC	are constrained to the most biologically active conformation. The	
CC	bridged molecules are up to 45 times more nuclease resistant than the	
CC	unbridged molecules. These sequences can be used as diagnostic probes	

CC to monitor the presence of thrombin, and thereby determine whether there
 CC is a need to modulate its function or activity. The inhibitors can also
 CC be administered to a cell in order to prevent the deleterious
 CC consequences of overproduction of thrombin, or to effect the benefits of
 CC inhibition of thrombin function.

XX Sequence 15 BP; 0 A; 0 C; 9 G; 6 T; 0 other;

Query Match 100.0%; Score 15; DB 17; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 GY 1 ggttggtgtgtgtg 15
 |||||
 Db 1 ggttggtgtgtgtg 15

RESULT 13

AA17808 standard; DNA; 15 BP.

AA17808;

30-OCT-1996 (first entry)

Glycosaminoglycan-degrading enzyme inhibitor LG1PS.

Glycosaminoglycan-degrading enzyme; GDE; inhibitor; endoglycosidase;
 heparinase; heparitinase; mammalian; bacterial; platelet; macrophage;
 neutrophil; leukocyte; endothelial cell; smooth muscle cell; carcinoma;
 tumor cell; activation; proliferation; migration; cancer; inflammation;
 autoimmune disorder; infection; pathogenic organism; atherosclerosis;
 cardiovascular disease; vascular hyperplasia; restenosis; therapy; ss.

Synthetic.

Key Location/Qualifiers
 modified_base 1..15
 /*tag= a "optionally phosphorothioated, or
 /note= phosphorodithioated backbone"

W09608559-A1.

21-MAR-1996.

13-SEP-1995; 95MO-AU00600.

14-AUG-1995; 95AU-0004769.

16-SEP-1994; 94AU-0008226.

16-SEP-1994; 94AU-0008227.

(CARD-) CARDIAC CRC NOMINEES PTY LTD.

Graham L, Underwood PA;

WPI: 1996-179936/18.

Oligo:nucleotide(s) having sulphur substs. between nucleoside(s) -
 for inhibiting glycosaminoglycan-degrading enzymes, for treating,
 e.g. cancer, inflammation, infection or autoimmune disorders.

Example 2; Page 33; 73pp; English.

AA17805-117808, and AA17810-117813 represent
 glycosaminoglycan-degrading enzyme (GDE) inhibitors. The GDEs which
 these sequences inhibit are endoglycosidases (which cleave
 glycosaminoglycan chains at internal sites), preferably heparanases (also
 known as heparinases) of mammalian or bacterial origin. These
 sequences can be used for inhibiting GDEs associated with platelets,
 macrophages, neutrophils, leukocytes, endothelial cells, smooth muscle
 cells, carcinoma and tumor cells, and bacteria. They can also be used

CC to inhibit smooth muscle cell activation, proliferation or migration.
 CC The sequences can be used to treat cancer, inflammation, autoimmune
 CC disorders, infection caused by pathogenic organisms, and cardiovascular
 CC disease, such as vascular hyperplasia, restenosis and atherosclerosis.
 CC These inhibitors can also be used as biochemical reagents for studying
 CC GDE activities and mechanisms of enzyme activity.

XX Sequence 15 BP; 0 A; 0 C; 9 G; 6 T; 0 other;

Query Match 100.0%; Score 15; DB 17; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 GY 1 ggttggtgtgtgtg 15
 |||||
 Db 1 ggttggtgtgtgtg 15

RESULT 14

AA51669 standard; DNA; 15 BP.

AA51669;

12-NOV-1997 (first entry)

Viral integrase inhibiting oligonucleotide.

Human immunodeficiency virus; HIV; Epstein Barr virus; EBV;
 herpes simplex virus; HSV; human papilloma virus; HPV; adenovirus;
 respiratory syncytial virus; RSV; cytomegalovirus; CMV; hepatitis B;
 integrase inhibition; guanosine tetrad; ss.

Synthetic.

Key Location/Qualifiers
 modified_base 1..15
 /*tag= a "optionally contains all phosphorothioate
 /note= linkages or a phosphorothioate linkage
 between penultimate and last nucleotide
 at 3' end"

W09703997-A1.

06-FEB-1997.

17-JUL-1996; 96MO-US11786.

23-APR-1996; 96US-0016271.

19-JUL-1995; 95US-0001505.

23-OCT-1995; 95US-0535168.

19-MAR-1996; 96US-0013688.

25-MAR-1996; 96US-0014007.

17-APR-1996; 96US-0015714.

(ARON-) ARONEX PHARM INC.

Fennwald S, Hogan ME, Mazumder A, O'wang JO, Pommer Y;

Rando RF, Zendequi JG;

WPI: 1997-132569/12.

Oligo:nucleotide(s) capable of forming guanosine tetrads - inhibit
 viral enzyme responsible for integrating viral nucleic acid into the
 host genome

Claim 3; Page 81; 245pp; English.

AA51619-T51698 are oligonucleotides used to inhibit the production
 of viruses within a host cell. The oligonucleotides may form guanosine
 tetrads (structures formed of eight hydrogen bonds by coordination of

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 6, 2002, 15:32:59 ; Search time 51.8 Seconds
(without alignments)
71.129 Million cell updates/sec

Title: US-09-599-220-1

Perfect score: 15
Sequence: 1 ggttggtgtgtgtg 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 543772

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCITUS.COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	1	US-07-973-333-1
2	15	100.0	15	1	US-08-219-012-1
3	15	100.0	15	1	US-08-376-329-1
4	15	100.0	15	1	US-08-276-271-1
5	15	100.0	15	1	US-08-539-516-4
6	15	100.0	15	1	US-08-614-447-4
7	15	100.0	15	1	US-08-703-755A-3
8	15	100.0	15	1	US-08-484-192-29
9	15	100.0	15	1	US-08-484-192-31
10	15	100.0	15	1	US-08-484-192-32
11	15	100.0	15	1	US-08-484-192-36
12	15	100.0	15	1	US-08-484-192-37
13	15	100.0	15	1	US-08-484-192-38
14	15	100.0	15	1	US-08-484-192-79
15	15	100.0	15	2	US-08-237-973-19
16	15	100.0	15	2	US-08-237-973-21
17	15	100.0	15	2	US-08-237-973-22
18	15	100.0	15	2	US-09-007-227-1
19	15	100.0	15	2	US-09-007-227-4
20	15	100.0	15	3	US-08-910-632-81
21	15	100.0	15	4	US-08-687-421-189
22	15	100.0	15	4	US-09-017-974-53
23	15	100.0	15	4	US-09-429-130-53
24	15	100.0	15	5	PCT-US94-00896-1
25	15	100.0	15	5	PCT-US95-09237-1
26	15	100.0	15	5	PCT-US95-11985A-21
27	15	100.0	17	1	US-08-234-613-32

28	15	100.0	17	1	US-08-234-613-46	Sequence 46, Appl
29	15	100.0	17	1	US-08-484-192-30	Sequence 30, Appl
30	15	100.0	17	1	US-08-484-192-104	Sequence 104, App
31	15	100.0	17	1	US-08-484-192-118	Sequence 118, App
32	15	100.0	17	2	US-08-237-973-20	Sequence 20, Appl
33	15	100.0	17	2	US-08-237-973-45	Sequence 45, Appl
34	15	100.0	17	2	US-08-237-973-59	Sequence 59, Appl
35	15	100.0	17	4	US-09-017-974-54	Sequence 54, Appl
36	15	100.0	17	4	US-09-429-130-54	Sequence 55, Appl
37	15	100.0	18	4	US-09-017-974-55	Sequence 55, Appl
38	15	100.0	31	3	US-09-429-130-55	Sequence 55, Appl
39	15	100.0	31	3	US-08-910-632-83	Sequence 83, Appl
40	15	100.0	36	5	PCT-US95-11985A-29	Sequence 29, Appl
41	15	100.0	39	2	US-09-007-227-2	Sequence 2, Appl
42	15	100.0	39	2	US-09-007-227-3	Sequence 3, Appl
43	15	100.0	40	4	US-09-287-936-6	Sequence 6, Appl
44	15	100.0	44	1	US-08-703-755A-7	Sequence 7, Appl
45	14	93.3	15	1	US-08-484-192-35	Sequence 35, Appl

ALIGNMENTS

```
RESULT 1
US-07-973-333-1
; Sequence 1, Application US/07973333
; Patent No. 5476766
; GENERAL INFORMATION:
; APPLICANT: Larry Gold
; APPLICANT: Diane Tasset
; TITLE OF INVENTION: Ligands of Thrombin
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beaton & Swanson, P.C.
; STREET: 4582 South Ulster Street Parkway, Suite#
; STREET: 403
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80237
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/973,333
; FILING DATE: 19921106
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: none
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 850-9900
; TELEFAX: (303) 850-9401
; INFORMATION FOR SEQ. ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-973-333-1

Query Match      100.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
US-08-219-012-1
; Sequence 1, Application US/08219012
; Patent No. 5543293
; GENERAL INFORMATION:
; APPLICANT: Larry Gold
; APPLICANT: Diane Tasset
; TITLE OF INVENTION: Ligands of Thrombin
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beaton & Swanson, P.C.
; STREET: 4582 South Ulster Street Parkway, Suite #
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80237
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/219,012
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: none
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 850-9900
; TELEFAX: (303) 850-9401
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-08-219-012-1

Query Match 100.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggttggtgtgttg 15
Db 1 ggttggtgtgttg 15

RESULT 3
US-08-376-329-1
; Sequence 1, Application US/08376329
; Patent No. 5641629
; GENERAL INFORMATION:
; APPLICANT: Pitner, James B
; APPLICANT: Malinowski, Douglas P
; APPLICANT: Vonk, Glenn P
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: Spectroscopically Detectable Nucleic
; TITLE OF INVENTION: Acid Ligands
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard J. Roderick, Becton Dickinson and
; COMPANY: Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: NJ
; COUNTRY: USA
```

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ZIP: 07417-1880
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/376,329
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hignett, David W
; REGISTRATION NUMBER: 30,265
; REFERENCE/DOCKET NUMBER: P-3126
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 847 5317
; TELEFAX: 201 848 9228
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULAR TYPE: DNA (genomic)
;
; US-08-376-329-1

Query Match 100.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggttggtgtgttg 15
Db 1 ggttggtgtgttg 15

RESULT 4
US-08-276-271-1
; Sequence 1, Application US/08276271
; Patent No. 5650275
; GENERAL INFORMATION:
; APPLICANT: Pitner, James B
; APPLICANT: Malinowski, Douglas P
; APPLICANT: Vonk, Glenn P
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: Spectroscopically Detectable Nucleic
; TITLE OF INVENTION: Acid Ligands
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard J. Roderick, Becton Dickinson and
; COMPANY: Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: NJ
; COUNTRY: USA
; ZIP: 07417-1880
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,271
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Hignett, David W
; REGISTRATION NUMBER: 30,265
; REFERENCE/DOCKET NUMBER: P-3126
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 847 5317
; TELEFAX: 201 848 9228
; INFORMATION FOR SEQ ID NO: 1:
```


ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
ADDRESS: Company
STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: NJ
COUNTRY: US
ZIP: 07417
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/703,755A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-3376
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-703-755A-3

Query Match 100.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggttggtggttg 15
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DB 1 ggttggtggttg 15

RESULT 8
US-08-484-192-29
Sequence 29, Application US/08484192
Patent No. 5756291
GENERAL INFORMATION:
APPLICANT: GRIFFIN, LINDA C.
APPLICANT: ALBRECHT, GLENN
APPLICANT: LATHAM, JOHN
APPLICANT: LEUNG, LAWRENCE
APPLICANT: VERMAAS, ERIC
APPLICANT: TOOLE, JOHN J.
TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND
METHODS OF MAKING
NUMBER OF SEQUENCES: 181
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,192
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,387
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: GRACEY, NANCY J.

REGISTRATION NUMBER: 28,216
REFERENCE/DOCKET NUMBER: 246102002221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-484-192-29

Query Match 100.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggttggtggttg 15
|||||
DB 1 ggttggtggttg 15

RESULT 9
US-08-484-192-31
Sequence 31, Application US/08484192
Patent No. 5756291
GENERAL INFORMATION:
APPLICANT: GRIFFIN, LINDA C.
APPLICANT: ALBRECHT, GLENN
APPLICANT: LATHAM, JOHN
APPLICANT: LEUNG, LAWRENCE
APPLICANT: VERMAAS, ERIC
APPLICANT: TOOLE, JOHN J.
TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND
METHODS OF MAKING
NUMBER OF SEQUENCES: 181
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,192
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,387
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: GRACEY, NANCY J.
REGISTRATION NUMBER: 28,216
REFERENCE/DOCKET NUMBER: 246102002221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: misc_difference

LOCATION: replace(13..15, "")
OTHER INFORMATION: /note="These positions are thioate
OTHER INFORMATION: (1.e., P(O)S) linked."
US-08-484-192-31

Query Match 100.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggttggtggttg 15
|||||
Db 1 GGTGGTGGTGG 15

RESULT 10
US-08-484-192-32
Sequence 32, Application US/08484192
Patent No. 5756291

GENERAL INFORMATION:

APPLICANT: GRIFFIN, LINDA C.

APPLICANT: ALBRECHT, GLENN

APPLICANT: LATHAM, JOHN

APPLICANT: LEUNG, LAWRENCE

APPLICANT: VERMAAS, ERIC

APPLICANT: TOOLE, JOHN J.

TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND

TITLE OF INVENTION: METHODS OF MAKING

NUMBER OF SEQUENCES: 181

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 PAGE MILL ROAD

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,192

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/934,387

FILING DATE: 21-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: GRACEY, NANCY J.

REGISTRATION NUMBER: 28,216

REFERENCE/DOCKET NUMBER: 246102002221

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-813-5600

TELEFAX: 415-494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: misc.difference

LOCATION: replace(1..15, "")

OTHER INFORMATION: /note="These positions are thioate

OTHER INFORMATION: (1.e., P(O)S) linked."

US-08-484-192-32

Query Match 100.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggttggtggttg 15
|||||
Db 1 GGTGGTGGTGG 15

RESULT 11
US-08-484-192-36
Sequence 36, Application US/08484192
Patent No. 5756291

GENERAL INFORMATION:

APPLICANT: GRIFFIN, LINDA C.

APPLICANT: ALBRECHT, GLENN

APPLICANT: LATHAM, JOHN

APPLICANT: LEUNG, LAWRENCE

APPLICANT: VERMAAS, ERIC

APPLICANT: TOOLE, JOHN J.

TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND

TITLE OF INVENTION: METHODS OF MAKING

NUMBER OF SEQUENCES: 181

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 PAGE MILL ROAD

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,192

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/934,387

FILING DATE: 21-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: GRACEY, NANCY J.

REGISTRATION NUMBER: 28,216

REFERENCE/DOCKET NUMBER: 246102002221

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-813-5600

TELEFAX: 415-494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: misc.difference

LOCATION: replace(3..4, "")

OTHER INFORMATION: /note="This is a formacetal

OTHER INFORMATION: linkage."

US-08-484-192-36

Query Match 100.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggttggtggttg 15
|||||
Db 1 GGTGGTGGTGG 15

RESULT 12
US-08-484-192-37
Sequence 37, Application US/08484192

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; Patent No. 5756291
; GENERAL INFORMATION:
; APPLICANT: GRIFFIN, LINDA C.
; APPLICANT: ALBRECHT, GLENN
; APPLICANT: LATHAM, JOHN
; APPLICANT: LEUNG, LAWRENCE
; APPLICANT: VERMAAS, ERIC
; APPLICANT: TOOLE, JOHN J.
; TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND
; NUMBER OF SEQUENCES: 181
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,192
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,387
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: GRACEY, NANCY J.
; REGISTRATION NUMBER: 28,216
; REFERENCE/DOCKET NUMBER: 246102002221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc_difference
; LOCATION: replace(12..13, "")
; OTHER INFORMATION: /note="This is a formacetal
; OTHER INFORMATION: linkage."
;
US-08-484-192-37

Query Match          100.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13
; US-08-484-192-38
; Sequence 38, Application US/08484192
; Patent No. 5756291
; GENERAL INFORMATION:
; APPLICANT: GRIFFIN, LINDA C.
; APPLICANT: ALBRECHT, GLENN
; APPLICANT: LATHAM, JOHN
; APPLICANT: LEUNG, LAWRENCE
; APPLICANT: VERMAAS, ERIC
; APPLICANT: TOOLE, JOHN J.
; TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND
; NUMBER OF SEQUENCES: 181
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,192
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,387
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: GRACEY, NANCY J.
; REGISTRATION NUMBER: 28,216
; REFERENCE/DOCKET NUMBER: 246102002221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc_difference
; LOCATION: replace(3..4, "")
; OTHER INFORMATION: /note="This is a formacetal
; OTHER INFORMATION: linkage."
;
US-08-484-192-38

Query Match          100.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14
; US-08-484-192-79
; Sequence 79, Application US/08484192
; Patent No. 5756291
; GENERAL INFORMATION:
; APPLICANT: GRIFFIN, LINDA C.
; APPLICANT: ALBRECHT, GLENN
; APPLICANT: LATHAM, JOHN
; APPLICANT: LEUNG, LAWRENCE
; APPLICANT: VERMAAS, ERIC
; APPLICANT: TOOLE, JOHN J.
; TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND
; NUMBER OF SEQUENCES: 181
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,192
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,387
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: GRACEY, NANCY J.
; REGISTRATION NUMBER: 28,216
; REFERENCE/DOCKET NUMBER: 246102002221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc_difference
; LOCATION: replace(12..13, "")
; OTHER INFORMATION: /note="This is a formacetal
; OTHER INFORMATION: linkage."
;
US-08-484-192-38
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; TITLE OF INVENTION: METHODS OF MAKING
; NUMBER OF SEQUENCES: 181
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,192
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,387
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: GRACEY, NANCY J.
; REGISTRATION NUMBER: 28,216
; REFERENCE/DOCKET NUMBER: 246102002221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc_difference
; LOCATION: replace(3..4, "")
; OTHER INFORMATION: /note="This is a formacetal
; OTHER INFORMATION: linkage."
;
US-08-484-192-38

Query Match          100.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14
; US-08-484-192-79
; Sequence 79, Application US/08484192
; Patent No. 5756291
; GENERAL INFORMATION:
; APPLICANT: GRIFFIN, LINDA C.
; APPLICANT: ALBRECHT, GLENN
; APPLICANT: LATHAM, JOHN
; APPLICANT: LEUNG, LAWRENCE
; APPLICANT: VERMAAS, ERIC
; APPLICANT: TOOLE, JOHN J.
; TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND
; NUMBER OF SEQUENCES: 181
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,192
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,387
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: GRACEY, NANCY J.
; REGISTRATION NUMBER: 28,216
; REFERENCE/DOCKET NUMBER: 246102002221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc_difference
; LOCATION: replace(12..13, "")
; OTHER INFORMATION: /note="This is a formacetal
; OTHER INFORMATION: linkage."
;
US-08-484-192-38
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STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,192
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,387
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: GRACEY, NANCY J.
REGISTRATION NUMBER: 28,216
REFERENCE/DOCKET NUMBER: 246102002221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: misc_difference
LOCATION: replace(13..15, "")
OTHER INFORMATION: /note="These positions are linked
OTHER INFORMATION: by thioate internucleotide linkages."
US-08-484-192-79

Query Match 100.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggttggtgtgttg 15
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Db 1 ggttggtgtgttg 15

RESULT 15
US-08-237-973-19
Sequence 19, Application US/08237973
Patent No. 5840867
GENERAL INFORMATION:
APPLICANT: TOOLE, JOHN J.
APPLICANT: LATHAM, JOHN
APPLICANT: BOCK, LOUIS C.
APPLICANT: GRIFFIN, LINDA C.
TITLE OF INVENTION: APTAMER ANALOGS SPECIFIC FOR
TITLE OF INVENTION: BIOMOLECULES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/237,973
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,921
FILING DATE: 06-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: GRACEY, NANCY J.
REGISTRATION NUMBER: 28,216
REFERENCE/DOCKET NUMBER: 24610-20032.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-237-973-19

Query Match 100.0%; Score 15; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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